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ATP synthase F1, gamma subunit [ATPG] [Shewanella onei... 385 e-106

ATP synthase gamma subunit protein (EC 3.6.1.34) (Memb... 381 e-105

ATP synthase gamma subunit [STY3912] [Salmonella typhi]

tr Q8E8B9

T tr Q8Z9S5

tr Q8Z2Q5

```
ATP synthase F1, gamma subunit [VC2765] [Vibrio cholerae] 376 e-103
tr Q9KNH4
tr Q7MGH9
               FOF1-type ATP synthase, gamma subunit [VV3252] [Vibrio... 375 e-103
              ATP synthase F1, gamma subunit [VV11020] [Vibrio vulni... 375 e-103
□ tr Q8DDG9
              ATP synthase F1, gamma subunit [VP3070] [Vibrio paraha... 374 e-102
___ tr Q87KA7
sp P12990
               ATPG VIBAL ATP synthase gamma chain (EC 3.6.3.14) [ATP... 373 e-102
T tr Q9HT19
               ATP synthase gamma chain [ATPG] [Pseudomonas aeruginosa] 362 5e-99
T tr <u>Q8VV78</u>
               FOF1-ATPase subunit gamma [ATPG] [Colwellia maris (Vib... 353 2e-96
tr Q88BX3
               ATP synthase F1, gamma subunit [ATPG] [Pseudomonas put... 349 2e-95
               ATP synthase F1, gamma subunit [ATPG] [Pseudomonas syr... 347 9e-95
tr Q87TT3
tr Q83AF6
               ATP synthase, F1 gamma subunit [ATPG] [Coxiella burnetii] 338 4e-92
tr Q82XP9
               ATP synthase gamma subunit (EC 3.6.3.14) [ATPG] [Nitro... 337 le-91

    □ tr Q8XU75

               Probable ATP synthase gamma chain protein (EC 3.6.1.34... 331 9e-90
               ATP synthase gamma chain [ATPG] [Xanthomonas campestri... 323 2e-87
tr Q8PCZ6
Sp 051873
               ATPG BUCAP ATP synthase gamma chain (EC 3.6.3.14) [ATP... 322 3e-87
               ATPG BUCAI ATP synthase gamma chain (EC 3.6.3.14) [ATP... 322 3e-87
sp P57123
               ATP synthase gamma chain [ATPG] [Xanthomonas axonopodi... 318 5e-86
tr Q8PGG6
               ATP synthase gamma chain [ATPG] [Xylella fastidiosa (s... 305 5e-82
T tr Q87E89
☐ tr Q9PE84
               ATP synthase, gamma chain [XF1144] [Xylella fastidiosa]
                                                                        305 5e-82
               ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Bordete... 304 9e-82
tr Q7VU45
tr Q7WEM8
               ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Bordete... 304 1e-81
               ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Bordete... 303 2e-81
☐ tr Q7W3A9
               ATP synthase gamma subunit (EC 3.6.3.14) [ATPG] [Candi... 302 3e-81
□ tr Q7VQV7
sp P41169
               ATPG THIFE ATP synthase gamma chain (EC 3.6.3.14) [ATP... 301 8e-81
T tr Q7P096
               H+-transporting two-sector ATPase, gamma subunit (EC 3... 300 2e-80
               ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Hae... 297 1e-79
T tr Q83U82
               ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Hae... 296 2e-79
T tr Q83V88
T tr Q83V83
               ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Hae... 296 2e-79
               ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Hae... 295 4e-79
☐ tr Q83V86
tr Q9RQ80
               Gamma subunit of membrane-bound ATP synthase [ATPG] [B... 295 4e-79
tr Q9JW71
               ATP synthase gamma chain (EC 3.6.1.34) [ATPG] [Neisser... 295 5e-79
               ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Hae... 295 5e-79
_____tr Q83U83
               ATP synthase F1, gamma subunit [NMB1935] [Neisseria me... 295 7e-79
ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Hae... 294 9e-79
T tr Q83V85
               ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Hae... 294 le-78
☐ tr Q83V87
               ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Hae... 293 2e-78
tr Q83UA6
               ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Hae... 293 2e-78
T tr Q83V84
T tr Q83V89
               ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Hae... 292 4e-78
               Gamma subunit of membrane-bound ATP synthase [ATPG] [B... 268 9e-71
tr Q9RQ74
tr Q8D3J4
               AtpG protein [ATPG] [Wigglesworthia glossinidia brevip... 265 8e-70
               ATPG BUCBP ATP synthase gamma chain (EC 3.6.3.14) [ATP... 261 9e-69
Sp Q89B40
tr Q9RQ77
               Gamma subunit of membrane-bound ATP synthase [ATPG] [B... 256 3e-67
               ATP synthase F1, gamma subunit [ATPG] [Enterococcus fa... 218 8e-56
T tr Q831A4
               ATPG BACME ATP synthase gamma chain (EC 3.6.3.14) [ATP... 216 4e-55
☐ sp P20602
tn AAQ10089 ATP synthase subunit gamma [ATPG] [Bacillus sp. TA2.A1]
tr Q8E5U9
               H+-transporting ATP synthase gamma chain [ATPG] [Strep... 210 2e-53
```

П	sp	Q9K6H4	ATPG BACHD ATP synthase gamma chain (EC 3.6.3.14) [ATP	209	4e-53
	_	Q8E073	ATP synthase F1, gamma subunit [ATPG] [Streptococcus a	208	9e-53
	tr	Q814W1	ATP synthase gamma chain (EC 3.6.3.14) [BC5307] [Bacil		
	tr	Q81JZ4	ATP synthase F1, gamma subunit [ATPG] [Bacillus anthra	207	1e-52
	tn	AAS44331	ATP synthase F1, gamma subunit (EC 3.6.3.14) [ATPG]	207	1e-52
	tr	Q9RAU1	H+-ATPase cytoplasmic F1-part gamma-subunit (H+-ATPase	206	3e-52
	tr	Q8EM82	H(+)-transporting ATP synthase gamma chain (EC 3.6.1.3	206	4e-52
ГТ	sp	Q9CER9	ATPG_LACLA ATP synthase gamma chain (EC 3.6.3.14) [ATP	205	7e-52
	sp	P22482	ATPG_BACPF ATP synthase gamma chain (EC 3.6.3.14) [ATP	205	7e-52
	tr	Q8CNJ6	ATP synthase gamma chain [SE1701] [Staphylococcus epid	205	7e-52
	tr	005432	ATP synthase subunit gamma [ATPG] [Moorella thermoacet	204	1e-51
-	sp	P09222	ATPG_BACP3 ATP synthase gamma chain precursor (EC 3.6	202	6e-51
J., st.	tr	Q9A0I8	Putative proton-translocating ATPase, gamma subunit (E	201	8e-51
[]	tr	Q52412	TF1-gamma subunit [thermophilic bacterium PS3]	201	1e-50
	sp	P37810	ATPG_BACSU ATP synthase gamma chain (EC 3.6.3.14) [ATP	201	1e-50
	tr	Q99SF4	ATP synthase gamma chain [ATPG] [Staphylococcus aureus	201	1e-50
	tr	050158	Proton-translocating ATPase, gamma subunit [ATPG] [Str	201	1e-50
	tr	Q8K827	Putative proton-translocating ATPase gamma subunit [SP	200	2e-50
	tr	Q84XB4	Chloroplast ATPase gamma subunit precursor [ATPC] [Pha	200	2e-50
	sp	P12408	ATPG_ANASP ATP synthase gamma chain (EC 3.6.3.14) [ATP	198	9e-50
	sp	P41010	ATPG_BACCA ATP synthase gamma chain (EC 3.6.3.14) [ATP	197	2e-49
	sp	P42007	ATPG_BACST ATP synthase gamma chain (EC 3.6.3.14) [ATP	196	3e-49
	tr	Q927W3	AtpG protein [ATPG] [Listeria monocytogenes, Listeria	195	6e-49
	sp	P29710	ATPG_PROMO ATP synthase gamma chain, sodium ion specif	194	2e-48
	sp	Q41075	ATPG_PHATR ATP synthase gamma chain, chloroplast precu	194	2e-48
[]	sp	Q06908	ATPG_ODOSI ATP synthase gamma chain, chloroplast precu	194	2e-48
	tr	Q8FQ21	H+-ATPase gamma subunit (EC 3.6.3.14) [ATPG] [Coryneba	194	2e-48
	tr	Q8KRU9	Subunit gamma [ATPG] [Ilyobacter tartaricus]	194	2e-48
	sp	P43452	ATPG_ENTHR ATP synthase gamma chain (EC 3.6.3.14) [ATP	<u>193</u>	3e-48
Town I	tr	Q8KAW9	ATP synthase F1, gamma subunit [ATPG] [Chlorobium tepi	192	5e-48
w/(2) es	tr	Q8RKV3	$\label{eq:H+-ATPase} \mbox{ H+-ATPase cytoplasmic F1-part gamma-subunit [ATPG] [St}$	192	5e-48
Ī	sp	P08450	ATPG_SYNP6 ATP synthase gamma chain (EC 3.6.3.14) [ATP	<u>191</u>	8e-48
	sp	Q05384	ATPG_SYNP1 ATP synthase gamma chain (EC 3.6.3.14) [ATP	191	1e-47
50.5	tr	Q8DLU1	H+-transporting ATP synthase gamma chain [ATPC] [Synec	191	1e-47
	sp	P17253	ATPG_SYNY3 ATP synthase gamma chain (EC 3.6.3.14) [ATP	190	2e-47
	tr	Q7NDC0	ATP synthase gamma chain [ATPC] [Gloeobacter violaceus]	190	2e-47
	sp	P50005	ATPG_ACEWO ATP synthase gamma chain, sodium ion specif		
	tr	Q7P5L4	ATP synthase gamma chain, sodium ion specific (EC 3.6	<u>189</u>	4e-47
	tr	Q97PT5	ATP synthase F1, gamma subunit (Proton-translocating A	189	5e-47
	tr	Q8RGE1	ATP synthase gamma chain, sodium ion specific (EC 3.6	187	1e-46
	tr	Q7MA19	ATP synthase F1 gamma subunit (EC 3.6.3.14) [ATPG] [Wo	187	2e-46
		Q9ZJ02	Proton-translocating ATPase gamma subunit [Streptococc		
		Q9FDR6	H+-ATPase gamma subunit (F0F1-type ATP synthase gamma		
		Q9FAA4	H+-ATPase gamma subunit [ATPG] [Brevibacterium flavum]		4e-46
l _{ant} ,	tn	CAF19915	ATP SYNTHASE GAMMA SUBUNIT (EC 3.6.3.14) [ATPG] [Cor	186	4e-46

Graphical overview of the alignments

Click here

to resubmit your query after masking regions matching $\underline{\mathtt{PROSITE}}$ profiles or Pfam HMMs

(Help) (use ScanProsite for more details about PROSITE matches)

Profile hits
Pfam hits

ATP-synt

Matches on query sequence Hat Submission 100 150 200 250 1 ATPG_HAEIN ATPG_PASMU Q7VPP1 DESCRIPTION OF THE PERSON OF T (SECTION) ĂTPG ÉCOLI Q8ZK#8 (2) SEE 13 Q9RFL4 Diet. 07NA93 EEEE 3 Å8E8B9 THE STATE OF 08Z2Q5 Q8Z9S5 **FREE S** E E Q9KNH4 Same: Q7MGH9 Q8DDG9 alemanus (Õ87KA7 ATPG_VIBAL Q9HT19 FIGURE BURD Part Q8VV78 Secon Q88BX3 rare. Q87TT3 CHRON Q83AF6 4755735 Q82XP9 Q8XU75 ÕBPCZĞ ATPG_BUCAP ATPG_BUCAI Q8PGG6 6733 Q87E89 09PE84 07VU45 07HEH8 go co 07H3H9 07VQV7 27753 FT 713 ATPG_THIFE Q7P096 RETERM NAME OF THE PARTY Q83U82 編起/蘇末 ดีสวบสล 083V83 Q83V86 影響網接 Q9RQ80 (MATERIA) Q9JH71 Q83U83 09.IX01 0825 083785 Q83V87 Q83VA6 C TO SERVICE 083V84 083V89 ligavoler. Õ9RO74 ARREST C ดิชิ**ม**ริป4 0.000 ATPG_BUCBP Q9RQ77 SSTREET, ST (CONTRACT) Q831A4 0.023 ATPG_BACHE AAQ10089 2.55 G Q8È5U9 MARKET . ÃTPG_BACHD Q8E073 10020031 DESCRIPTION OF THE PARTY OF THE Q814H1 CELLO 081.JZ4 COMPANY. ÃÃŜ44331 PRODUCTION OF THE PARTY OF THE Q9RAU1 (0.655) Q8EH82 CHARLE ATPG_LACLA ATPG_BACPF Q8CNJ6 22001 6353 KREEDE 005432 Part 3 ĀŢŘĠĽBACP3 Q<u>9</u>AQĪ8 100000000 CHECK TO Q52412 CELL ATPG_BACSU 0995F4 E 22.29 GIZZ 050158 C77(43 Q8K827 F1123 Q84XB4 HALE. QOYADA ATPG_ANASP ATPG_BACCA ATPG_BACST Q927N3 ATPG_PROMO ATPG_PHATR ATPG_ODOSI 100 10.5% E **C** PER SE Lie III 08F021 50000000 Q8KRU9 And the second s 277329 ATPG_ENTHR Q8KAH9 CONT 1027 Q8RKV3 CESTO!

Alignments

sp P43716 ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Haemophilus 289 AA ATPG HAEIN influenzae] align Score = 562 bits (1448), Expect = e-159 Identities = 289/289 (100%), Positives = 289/289 (100%) Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS Sbjct: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60 Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNOIKNWKEONISTDLGLIGS 120 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS Sbjct: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120 Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS Sbjct: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180 Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS Sbjct: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240 Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI Sbjct: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289 sp Q9L6B6 ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Pasteurella 289 AA ATPG_PASMU multocida] align Score = 456 bits (1173), Expect = e-127 Identities = 221/289 (76%), Positives = 263/289 (90%) Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60 MAGAKEI+TKIASV+STQKITKAMEMVA SKMRKTQ+RM++SRPYSETIRNVISHVSKA+ Sbjct: 1 MAGAKEIRTKIASVKSTQKITKAMEMVAASKMRKTQERMSSSRPYSETIRNVISHVSKAT 60 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120 Query: 61 IGYKHPFLV+REVKK+G++V+STDRG+CGGLNVNLFKT LN++K WKE+++S L LIGS Sbjct: 61 IGYKHPFLVDREVKKVGMIVVSTDRGLCGGLNVNLFKTVLNEMKEWKEKDVSVQLSLIGS 120

- Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240 QKPV+++L+PLPE +D L ER+Q WDY+YEP+ KVLLD+LLVRYLESQ+YQA V+N+AS
- Sbjct: 181 QKPVLEKLIPLPELDNDELGERKQVWDYIYEPDAKVLLDNLLVRYLESQVYQAAVENLAS 240

Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180

Sbjct: 121 KSINFFQSLGIKILTQDSGIGDTPSVEQLIGSVNSMIDAYKKGEVDVVYLVYNKFINTMS 180

K I+FF+S G I Q SG+GDTP++E+LIG N+M DAY+ GE+D VY+ YNKF+NTMS

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289 EQAARMVAMKAATDNAGNLIN+L+LVYNKARQASITNELNEIVAGAAAI Sbjct: 241 EQAARMVAMKAATDNAGNLINELQLVYNKARQASITNELNEIVAGAAAI 289

288 AA tr O7VPP1 ATP synthase gamma chain [ATPG] [Haemophilus aliqn Score = 438 bits (1127), Expect = e-122Identities = 212/289 (73%), Positives = 259/289 (89%), Gaps = 1/289 (0%) MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60 Query: 1 MAGAKEI+TKIASV++TQKITKAMEMVATSKMRKTQ+RMAA RPYSETIR VISH++K S Sbjct: 1 MAGAKEIRTKIASVRNTQKITKAMEMVATSKMRKTQERMAAGRPYSETIRKVISHIAKGS 60 Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120 IGYKHPFL+ER+VKK+G LVISTDRG+CGGLN+NLFKTTLN+ K WK++++S +LGL+GS IGYKHPFLIERDVKKVGYLVISTDRGLCGGLNINLFKTTLNEFKAWKDKDVSVELGLVGS 120 Sbjct: 61 Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180 KG+SF++S G ++ ++GLGD+P +E ++G N M +AYRNGE+D V IAYN+F NTMS Sbjct: 121 KGVSFYQSIGLKVRAHITGLGDSPEMERIVGAVNEMINAYRNGEVDMVCIAYNRFENTMS 180 Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240 QK V+ QL+PLP+ ++D L E + +WDYLYEP P+VLLDSLL+RYLE+Q+YQAVVDN+AS Sbjct: 181 QKTVIAQLLPLPKLENDEL-ETKCSWDYLYEPNPQVLLDSLLIRYLETQVYQAVVDNLAS 239 Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289 EQAARMVAMKAATDNAG LI++L+LVYNKARQASITNELNEIVAGAAAI Sbjct: 240 EQAARMVAMKAATDNAGALIDELQLVYNKARQASITNELNEIVAGAAAI 288

sp P00837 ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Escherichia 287 ATPG_ECOLI coli, AA Escherichia coli 06, Escherichia coli 0157:H7, Shigella align flexneril

Score = 390 bits (1001), Expect = e-107Identities = 188/289 (65%), Positives = 237/289 (81%), Gaps = 2/289 (0%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60 MAGAKEI++KIASVQ+TQKITKAMEMVA SKMRK+QDRMAASRPY+ET+R VI H++ +

Sbjct: 1 MAGAKEIRSKIASVQNTQKITKAMEMVAASKMRKSQDRMAASRPYAETMRKVIGHLAHGN 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120 + YKHP+L +R+VK++G LV+STDRG+CGGLN+NLFK L ++K W ++ + DL +IGS

Sbjct: 61 LEYKHPYLEDRDVKRVGYLVVSTDRGLCGGLNINLFKKLLAEMKTWTDKGVQCDLAMIGS 120

Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180

KG+SFF S G N+ Q++G+GD P+L ELIG M AY G +D +YI NKF+NTMS
Sbjct: 121 KGVSFFNSVGGNVVAQVTGMGDNPSLSELIGPVKVMLQAYDEGRLDKLYIVSNKFINTMS 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQOTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240

Q P + QL+PLP S DD L + ++WDYLYEP+PK LLD+LL RY+ESQ+YQ VV+N+AS

Sbjct: 181 QVPTISQLLPLPASDDDDL--KHKSWDYLYEPDPKALLDTLLRRYVESQVYQGVVENLAS 238

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289

EQAARMVAMKAATDN G+LI +L+LVYNKARQASIT EL EIV+GAAA+
Sbjct: 239 EQAARMVAMKAATDNGGSLIKELQLVYNKARQASITQELTEIVSGAAAV 287

287 tr Q8ZKW8 Membrane-bound ATP synthase, F1 sector, gamma-subunit (EC 3.6.3.14) AA[ATPG] [Salmonella typhimurium] align Score = 389 bits (999), Expect = e-107 Identities = 188/289 (65%), Positives = 237/289 (81%), Gaps = 2/289 (0%) MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60 Query: 1 MAGAKEI++KIASVQ+TQKITKAMEMVA SKMRK+QDRMAASRPY+ET+R VI H++ + Sbjct: 1 MAGAKEIRSKIASVQNTQKITKAMEMVAASKMRKSQDRMAASRPYAETMRKVIGHLANGN 60 Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEONISTDLGLIGS 120 + YKHP+L ER+VK++G LV+STDRG+CGGLN+NLFK L +K W ++ + +L +IGS Sbjct: 61 LEYKHPYLEERDVKRVGYLVVSTDRGLCGGLNINLFKKLLADMKAWSDKGVQCELAMIGS 120 Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180 KG+SFF S G N+ Q++G+GD P+L ELIG M AY G +D +YI NKF+NTMS Sbjct: 121 KGVSFFNSVGGNVVAQVTGMGDNPSLSELIGPVKVMLQAYDEGRLDKLYIVSNKFINTMS 180 Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240 Q P + QL+PLP S+DD L +++ WDYLYEP+PK LLD+LL RY+ESQ+YQ VV+N+AS Sbjct: 181 QVPTITQLLPLPASEDDDL--KRKAWDYLYEPDPKALLDTLLRRYVESQVYQGVVENLAS 238 Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289 EQAARMVAMKAATDN G+LI +L+LVYNKARQASIT EL EIV+GAAA+

tr Q9RFL4 ATP synthase subunit gamma [ATPG] [Salmonella typhimurium] 287 AA

align

Score = 389 bits (999), Expect = e-107

Identities = 188/289 (65%), Positives = 237/289 (81%), Gaps = 2/289 (0%)

Sbjct: 239 EQAARMVAMKAATDNGGSLIKELQLVYNKARQASITQELTEIVSGAAAV 287

Identities = 188/289 (65%), Positives = 237/289 (81%), Gaps = 2/289 (0%)

MAGAKEI++KIASVQ+TQKITKAMEMVA SKMRK+QDRMAASRPY+ET+R VI H++ +

MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60

Sbjct: 1 MAGAKEIRSKIASVQNTQKITKAMEMVAASKMRKSQDRMAASRPYAETMRKVIGHLAHGN 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120 + YKHP+L +R+VK++G LV+STDRG+CGGLN+NLFK L ++K W ++ + DL +IGS

Sbjct: 61 LEYKHPYLEDRDVKRVGYLVVSTDRGLCGGLNINLFKKLLAEMKTWTDKGVQCDLAMIGS 120

Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180

RG+SFF S G N+ Q++G+GD P+L ELIG M AY G +D +YI NKF+NTMS

Sbjct: 121 KGVSFFDSVGGNVVAQVTGMGDNPSLSELIGPVKVMLQAYDEGRLDKLYIVSNKFINTMS 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
Q P + QL+PLP S DD L + ++WDYLYEP+PK LLD+LL RY+ESQ+YQ VV+N+AS

Sbjct: 181 QVPTISQLLPLPASDDDDL--KHKSWDYLYEPDPKALLDTLLRRYVESQVYQGVVENLAS 238

Query: 1

```
Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
           EQAARMVAMKAATDN G+LI +L+LVYNKARQASIT EL EIV+GAAA+
Sbjct: 239 EQAARMVAMKAATDNGGSLIKELQLVYNKARQASITQELTEIVSGAAAV 287
tr Q7NA93 ATP synthase gamma chain [ATPG] [Photorhabdus luminescens
                                                                           287
                                                                           AΑ
           laumondii)]
                                                                           aliqn
 Score = 387 \text{ bits } (994), Expect = e-106
 Identities = 188/289 (65%), Positives = 238/289 (82%), Gaps = 2/289 (0%)
Query: 1
           MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
           MAGAKEI+TKIASVQ+TQKITKAMEMVA SKMRKTQDRMAASRPY+ETIR+VI H++ +
Sbjct: 1
           MAGAKEIRTKIASVQNTQKITKAMEMVAASKMRKTQDRMAASRPYAETIRSVIGHLALGN 60
Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
           + YKHP+L ERE K++G LV+STDRG+CGGLN NLFK L+++K+W ++++ +L LIGS
Sbjct: 61 LEYKHPYLEERETKRVGYLVVSTDRGLCGGLNTNLFKKLLSEMKDWSDKDVQCELALIGS 120
Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
           K SFF S G N+ Q++G+GD P+L ELIG N M AY G +D +Y+ NKF+NTMS
Sbjct: 121 KATSFFASVGGNVVAQVTGMGDNPSLSELIGPVNIMLRAYDEGRLDKLYVVTNKFINTMS 180
Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
           Q+P + QL+PLP
                         D+ L ++++WDYLYEP+PK LLD LL RY+ESQ+YQ VV+N+AS
Sbjct: 181 QEPTITQLLPLPAGDDETL -- KKKSWDYLYEPDPKALLDILLRRYVESQVYQGVVENLAS 238
Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
           EQAARMVAMKAATDN G+LI +L+LVYNKARQASIT EL EIV+GA+A+
Sbjct: 239 EQAARMVAMKAATDNGGSLIKELQLVYNKARQASITQELTEIVSGASAV 287
tr Q8E8B9 ATP synthase F1, gamma subunit [ATPG] [Shewanella oneidensis] 286 AA
                                                                          align
Score = 385 \text{ bits (990)}, Expect = e-106
Identities = 183/289 (63%), Positives = 237/289 (81%), Gaps = 3/289 (1%)
Query: 1
          MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
           MAGAKEIKTKIASV++TQKIT AMEMVA SKMR+ Q+RMAASRPY+E++R VI HV++ S
Sbjct: 1
          MAGAKEIKTKIASVKNTQKITSAMEMVAASKMRRAQERMAASRPYAESMRKVIGHVAQGS 60
Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
           + YKHP+L RE K++G +V++TDRG+CGGLNVNLFK + +K+WKEO
Sbjct: 61 LEYKHPYLEVREAKRVGYIVVATDRGLCGGLNVNLFKKVVADVKSWKEQGAEFEFCPIGA 120
Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
           + + FF+SFG + Q SGLGD P L +LIG
                                           M +AY G++D +Y+ +NKFVNTM+
Sbjct: 121 RSVQFFKSFGGQVSAQASGLGDAPKLNDLIGTVQVMLEAYNEGKLDRLYVVFNKFVNTMT 180
Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
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Q PV++QL+PLP+S+DD + R WDY+YEP+PK LLD+LLVRY+ESQ+YQ VV+N+AS

Sbjct: 181 QTPVIEQLLPLPKSEDDEVAHR---WDYIYEPDPKALLDTLLVRYVESQVYQGVVENIAS 237

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289 EQAARMVAMKAATDNAG LI+DL+LVYNKARQA+IT EL+EIV+GA+A+ Sbjct: 238 EQAARMVAMKAATDNAGTLIDDLQLVYNKARQAAITQELSEIVSGASAV 286 tr Q8Z2Q5 ATP synthase gamma subunit [STY3912] [Salmonella 287 AA typhi] aliqn Score = 385 bits (989), Expect = e-106Identities = 187/289 (64%), Positives = 235/289 (80%), Gaps = 2/289 (0%) Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60 MAGAKEI++KIASVQ+TQKITKAMEMVA SKMRK+QDRMAASRPY+ET+R VI H++ + Sbjct: 1 MAGAKEIRSKIASVQNTQKITKAMEMVAASKMRKSQDRMAASRPYAETMRKVIGHLANGN 60 Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120 + YKHP+L ER+VK++G LV+STD G+CGGLN+NLFK L +K W ++ + +L +IGS Sbjct: 61 LEYKHPYLEERDVKRVGYLVVSTDCGLCGGLNINLFKKLLADMKAWSDKGVQCELAMIGS 120 Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180 KG+SFF S G N+ Q++G+GD P+L ELIG M AY G +D +YI NKF+NTMS Sbjct: 121 KGVSFFNSVGGNVVAQVTGMGDNPSLSELIGPVKVMLQAYDEGRLDKLYIVSNKFINTMS 180 Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240 Q P + QL+PLP S+DD L ++ WDYLYEP+PK LLD+LL RY+ESO+YO VV+N+AS Sbjct: 181 QVPTITQLLPLPASEDDDL--KRTAWDYLYEPDPKALLDTLLRRYVESQVYQGVVENLAS 238 Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289 EQAARMVAMKAATDN G+LI +L+LVYNKARQASIT EL EIV+GAAA+ Sbjct: 239 EQAARMVAMKAATDNGGSLIKELQLVYNKARQASITQELTEIVSGAAAV 287 tr Q8Z9S5 ATP synthase gamma subunit protein (EC 3.6.1.34) (Membrane-287 AA ATP synthase, F1 sector, gamma-subunit) [ATPG] [Yersinia aliqn pestis] Score = 381 bits (979), Expect = e-105

Identities = 186/289 (64%), Positives = 236/289 (81%), Gaps = 2/289 (0%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60 MAGAKEI++KIASVQ+TQKITKAMEMVA SKMRK+Q+RMAASRPY+ET+R+VI H++ +

Sbjct: 1 MAGAKEIRSKIASVQNTQKITKAMEMVAASKMRKSQERMAASRPYAETMRSVIGHLALGN 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120 + YKHP+L ER+VK++G LV+STDRG+CGGLN+NLFK L ++K W E+ + DL LIGS

Sbjct: 61 LEYKHPYLEERDVKRVGYLVVSTDRGLCGGLNINLFKRLLAEMKGWSEKGVECDLALIGS 120

Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180

K SFF S G I Q++G+GD P+L ELIG M AY G +D +YI NKF+NTMS

Sbjct: 121 KAASFFGSVGGKIVAQVTGMGDNPSLSELIGPVKVMLQAYDEGRLDKLYIVNNKFINTMS 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240 Q+P + QL+PLP ++D L ++++WDYLYEP+PK LLD+LL RY+ESQ+YQ VV+N+AS

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Sbjct: 181 QEPRIMQLLPLPPAEDGEL--KKKSWDYLYEPDPKALLDTLLRRYVESQVYQGVVENLAS 238
Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
           EQAARMVAMKAATDN G+LI +L+LVYNKARQASIT EL EIV GA+A+
Sbjct: 239 EQAARMVAMKAATDNGGSLIKELQLVYNKARQASITQELTEIVGGASAV 287
tr Q9KNH4 ATP synthase F1, gamma subunit [VC2765] [Vibrio cholerae] 288 AA
                                                                      aliqn
 Score = 376 bits (965), Expect = e-103
 Identities = 179/289 (61%), Positives = 233/289 (79%), Gaps = 1/289 (0%)
           MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
Query: 1
           MAGAKEI+TKI SV+STQKITKAMEMVA SKMR++QD M +SRPY++TIR VI HV+ AS
Sbjct: 1
           MAGAKEIRTKIGSVKSTQKITKAMEMVAASKMRRSQDAMESSRPYAQTIRKVIGHVANAS 60
Ouery: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNOIKNWKEONISTDLGLIGS 120
           + Y+HP+L ERE K++G ++ISTDRG+CGGLN+NLFK + ++ WKE+
Sbjct: 61 LEYRHPYLEEREAKRVGYIIISTDRGLCGGLNINLFKKAITDMQTWKEKGAQIELAIIGS 120
Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
           K +FF + G + Q+SGLGD+P+LE+LIG
                                           M
                                                 Y = GE+D + Y+ + N+FVNTM
Sbjct: 121 KATAFFNNSGAKVAAQVSGLGDSPSLEDLIGSVGVMLKKYDKGELDRLYLVFNQFVNTMV 180
Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
           QKP + QL+PLP+S + + +R
                                   WDY+YEPEPK LLD+LL+R++ESQ+YQ VV+N+A
Sbjct: 181 QKPKIDQLLPLPKSDSEDM-QRDHMWDYIYEPEPKPLLDALLLRFIESQVYQGVVENLAC 239
Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
           EQAARMVAMKAATDNA NLI+DL+LVYNKARQA+IT EL+EIV GAAA+
Sbjct: 240 EQAARMVAMKAATDNASNLIDDLQLVYNKARQAAITQELSEIVGGAAAV 288
tr Q7MGH9 F0F1-type ATP synthase, gamma subunit [VV3252] [Vibrio
                                                                           288
           vulnificus
                                                                           AΑ
           (strain YJ016)]
                                                                           align
Score = 375 \text{ bits } (964), \text{ Expect = } e-103
Identities = 180/289 (62%), Positives = 235/289 (81%), Gaps = 1/289 (0%)
Query: 1
           MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
           MAGAKEI++KI SV+STQKITKAMEMVA SKMR++QD M ASRPY+ET+R VI HV+ AS
Sbjct: 1
           MAGAKEIRSKIGSVKSTQKITKAMEMVAASKMRRSQDAMEASRPYAETMRKVIGHVANAS 60
Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
           + Y+HP+L ERE K++G ++ISTDRG+CGGLN+N+FK + ++ WKE+
Sbjct: 61 LEYRHPYLDEREAKRVGYIIISTDRGLCGGLNINVFKKAVTDMQAWKEKGAEVELAVIGS 120
Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
           K +FF+ G + Q+SGLGD+P+LE+LIG + M + Y GE+D +Y+ +NKFVNTM
Sbjct: 121 KATAFFKHGGAKVAAQVSGLGDSPSLEDLIGSVSVMLEKYDEGELDRLYLVFNKFVNTMV 180
Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
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Q+P + QL+PLP+S D +R+ +WDY+YEPEP+ LLD+LLVRY+ESQ+YQ VV+N+A Sbjct: 181 QQPTIDQLLPLPKS-DSKDMQREHSWDYIYEPEPQALLDALLVRYVESQVYQGVVENLAC 239 Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289 EQAARMVAMKAATDNA NLI+DL LVYNKARQA+IT EL+EIV GAAA+ Sbjct: 240 EQAARMVAMKAATDNATNLIDDLELVYNKARQAAITQELSEIVGGAAAV 288 tr Q8DDG9 ATP synthase F1, gamma subunit [VV11020] [Vibrio vulnificus] 288 AA aliqn Score = 375 bits (964), Expect = e-103 Identities = 180/289 (62%), Positives = 235/289 (81%), Gaps = 1/289 (0%) MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60 Query: 1 MAGAKEI++KI SV+STQKITKAMEMVA SKMR++QD M ASRPY+ET+R VI HV+ AS MAGAKEIRSKIGSVKSTOKITKAMEMVAASKMRRSQDAMEASRPYAETMRKVIGHVANAS 60 Sbjct: 1 Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120 + Y+HP+L ERE K++G ++ISTDRG+CGGLN+N+FK + ++ WKE+ Sbjct: 61 LEYRHPYLDEREAKRVGYIIISTDRGLCGGLNINVFKKAVTDMQAWKEKGAEVELAVIGS 120 Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180 K +FF+ G + Q+SGLGD+P+LE+LIG + M + Y GE+D +Y+ +NKFVNTM Sbjct: 121 KATAFFKHGGAKVAAQVSGLGDSPSLEDLIGSVSVMLEKYDEGELDRLYLVFNKFVNTMV 180 Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240 Q+P + QL+PLP+S D +R+ +WDY+YEPEP+ LLD+LLVRY+ESQ+YQ VV+N+A Sbjct: 181 QQPTIDQLLPLPKS-DSKDMQREHSWDYIYEPEPQALLDALLVRYVESQVYQGVVENLAC 239 Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289 EQAARMVAMKAATDNA NLI+DL LVYNKARQA+IT EL+EIV GAAA+ Sbjct: 240 EQAARMVAMKAATDNATNLIDDLELVYNKARQAAITQELSEIVGGAAAV 288 tr Q87KA7 ATP synthase F1, gamma subunit [VP3070] [Vibrio 288 parahaemolyticus] AA align Score = 374 bits (959), Expect = e-102Identities = 178/289 (61%), Positives = 231/289 (79%), Gaps = 1/289 (0%) Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60 MAGAKEI+ KI SV+STQKITKAMEMVA SKMR++QD M ASRPY+ET+R VI HV+ A+ Sbjct: 1 MAGAKEIRNKIGSVKSTQKITKAMEMVAASKMRRSQDAMEASRPYAETMRKVIGHVANAN 60 Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120 + Y+HP+L ERE K++G +++STDRG+CGGLN+N+FK + I+ WKE+ Sbjct: 61 LEYRHPYLEEREAKRVGYIIVSTDRGLCGGLNINVFKKAVTDIQTWKEKGAEIELAVIGS 120 Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180 +FF+ G + Q+SGLGD+P+LE+LIG Y GE+D +Y+ +NKFVNTM Sbjct: 121 KATAFFKHGGAKVAAQVSGLGDSPSLEDLIGSVGVMLKKYDEGELDRLYVVFNKFVNTMV 180

 ${\tt Query:~181~QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS~240}$

Q+P + QL+PLP+S D +R+ +WDY+YEPEPK LLD+LLVRY+ESQ+YQ VV+N+A

Sbjct: 181 QQPTIDQLLPLPKS-DSKEMQREHSWDYIYEPEPKPLLDTLLVRYVESQVYQGVVENLAC 239

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289

EQAARM+AMKAATDNA NLI DL LVYNKARQA+IT EL+EIV GA+A+

Sbjct: 240 EQAARMIAMKAATDNATNLIEDLELVYNKARQAAITQELSEIVGGASAV 288

sp P12990 ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Vibrio 288 AA ATPG VIBAL alginolyticus]

align

Score = 373 bits (958), Expect = e-102Identities = 175/289 (60%), Positives = 232/289 (79%), Gaps = 1/289 (0%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
MAGAKEI+ KI SV+STQKITKAMEMVA SKMR++QD M ASRPY+ET+R VI HV+ A+

Sbjct: 1 MAGAKEIRNKIGSVKSTQKITKAMEMVAASKMRRSQDAMEASRPYAETMRKVIGHVANAN 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120 + Y+HP+L ERE K++G +++STDRG+CGGLN+N+FK + ++ W+E+ +L ++GS

Sbjct: 61 LEYRHPYLEEREAKRVGYIIVSTDRGLCGGLNINVFKKAVTDMQTWREKGAEIELAVVGS 120

Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180 K +FF+ G + Q+SGLGD P+LE+LIG M Y GE+D +Y+ +NKFVNTM

Sbjct: 121 KATAFFKHGGAKVAAQVSGLGDNPSLEDLIGSVGVMLKKYDEGELDRLYVVFNKFVNTMV 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
Q+P + QL+PLP+S + + +R+ +WDY+YEPEPK LLD+LLVRY+ESQ+YQ VV+N+A

Sbjct: 181 QQPTIDQLLPLPKSDSEEM-QREHSWDYIYEPEPKPLLDTLLVRYVESQVYQGVVENLAC 239

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289 EQAARM+AMKAATDNA NLI+DL LVYNKARQA+IT EL+EIV GAAA+

Sbjct: 240 EQAARMIAMKAATDNATNLIDDLELVYNKARQAAITQELSEIVGGAAAV 288

tr <u>Q9HT19</u> ATP synthase gamma chain [ATPG] [Pseudomonas 286 AA aeruginosa] align

Score = 362 bits (928), Expect = 5e-99
Identities = 178/289 (61%), Positives = 225/289 (77%), Gaps = 3/289 (1%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60 MAGAKEI++KIAS++STQKIT AME VA SKMRK Q RMAA RPY+E IR VI H++ A+

Sbjct: 1 MAGAKEIRSKIASIKSTQKITNAMEKVAVSKMRKAQMRMAAGRPYAERIRQVIGHLANAN 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120 Y+HPF+VEREVK++G +V+S+DRG+CGGLN+NLFK+ + + ++EQ DL +IGS

Sbjct: 61 PEYRHPFMVEREVKRVGYIVVSSDRGLCGGLNINLFKSLVKDMSGYREQGAEIDLCVIGS 120

Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180 KG SFFRSFG N+ +S LG+ P++ +LIG M DAY G ID +++ NKFVNTM+

Sbjct: 121 KGASFFRSFGGNVVAAISHLGEEPSINDLIGSVKVMLDAYLEGRIDRLFVVSNKFVNTMT 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240 D L QKP V+QL+PL WDYLYEP+ K LLD LLVRY+ESQ+YQAVV+N A Sbjct: 181 QKPTVEQLIPLVADDDQELKHH---WDYLYEPDAKSLLDGLLVRYVESQVYQAVVENNAC 237 Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289 EQAARM+AMK ATDNAG LI+DL+L+YNKARQA+IT E++EIV GAAA+ Sbjct: 238 EQAARMIAMKNATDNAGELISDLQLIYNKARQAAITQEISEIVGGAAAV 286 tr Q8VV78 F0F1-ATPase subunit gamma [ATPG] [Colwellia maris (Vibrio sp. 287 AA (strain ABE-1))] align Score = 353 bits (906), Expect = 2e-96 Identities = 171/289 (59%), Positives = 223/289 (76%), Gaps = 3/289 (1%) Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60 MA KEIKTKIASV+ TOKIT AMEMVA SKMRK O+ MAASRPY+ IRNVI H++ Sbjct: 1 MAVGKEIKTKIASVKGTQKITSAMEMVAASKMRKAQEGMAASRPYATNIRNVIGHIALGN 60 Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120 + Y+HP++ ERE K++G +V+S+DRG+CGGLN+NLFK L + Sbjct: 61 LEYRHPYMDEREAKRVGYIVVSSDRGLCGGLNINLFKKVLADAAEKQASGAEVEFCVIGS 120 Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180 K + FF + G + Q + SGLGD + P + L + L + GM AY NGEID +++ YNKFVNTM+ Sbjct: 121 KATAFFNNMGAKVSAQISGLGDSPSLTDLVGSVAVMLKAYDNGEIDRLHVVYNKFVNTMT 180 Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240 Q+P + QL+PLP+S D+ ++ R WDY+YEP+ LLD LLVRY+ESQ+YQ VV+N+A Sbjct: 181 QEPTIDQLLPLPKSDDEAISHR---WDYIYEPDANSLLDQLLVRYIESQVYQGVVENIAC 237 Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289 EQA+RMV+MKAATDNAG+LI+DL+LVYNKARQA+IT EL EIVAGAAA+ Sbjct: 238 EQASRMVSMKAATDNAGDLIDDLQLVYNKARQAAITQELGEIVAGAAAV 286 tr <u>Q88BX3</u> ATP synthase F1, gamma subunit [ATPG] [Pseudomonas putida 286 (strain AΑ KT2440)] align Score = 349 bits (896), Expect = 2e-95 Identities = 173/289 (59%), Positives = 223/289 (76%), Gaps = 3/289 (1%) Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60 MAGAKEI++KIAS++STQKIT AME VA SKMRK Q RMAASRPY+E IR VI H++ A+ Sbjct: 1 MAGAKEIRSKIASIKSTQKITSAMEKVAVSKMRKAQMRMAASRPYAERIRQVIGHLANAN 60 Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120 Y+HPF++ER VK+ G +V+S+DRG+CGGLN NLFK + + +EQ + DL + IGSSbjct: 61 PEYRHPFMIERPVKRAGYIVVSSDRGLCGGLNTNLFKALVKDMSANREQGVEIDLCVIGS 120 Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180 KG +FFR FG N+ +S LG+ P++ +LIG M DAY +G ID + + NKF+NTM+ Sbjct: 121 KGATFFRIFGGNVVAAISHLGEEPSINDLIGSVKVMLDAYLDGRIDRLSVVSNKFINTMT 180

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Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
           QKP V+QLVPL + D L WDYLYEP+ K LLD L+VRY+ESQ+YQAVV+N A+
Sbjct: 181 QKPTVEQLVPLVATPDQDLKHH---WDYLYEPDAKELLDGLMVRYVESQVYQAVVENNAA 237
Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
           EQAARM+AMK ATDNAG+LI +L+L+YNKARQA+IT E++EIV GAAA+
Sbjct: 238 EQAARMIAMKNATDNAGDLIKELQLIYNKARQAAITQEISEIVGGAAAV 286
tr Q87TT3 ATP synthase F1, gamma subunit [ATPG] [Pseudomonas syringae
                                                                          286
           (pv.
                                                                          AΑ
           tomato)]
                                                                          align
 Score = 347 bits (891), Expect = 9e-95
 Identities = 170/289 (58%), Positives = 225/289 (77%), Gaps = 3/289 (1%)
Query: 1
          MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
          MAGAKEI++KIAS++STQKIT AME VA SKMRK Q RMAASRPY+E IR VI H++ A+
Sbjct: 1
          MAGAKEIRSKIASIKSTQKITSAMEKVAVSKMRKAQMRMAASRPYAERIRQVIGHLANAN 60
Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNOIKNWKEONISTDLGLIGS 120
             Y HPF++ER +K++G +V+S+DRG+CGGLN NLFKT + +
                                                        +E + DL ++GS
Sbjct: 61 PEYLHPFMIERPLKRVGYVVVSSDRGLCGGLNTNLFKTLVKDMAVNRENGVEIDLCVVGS 120
Query: 121 KGISFFRSFGFNIKGOLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
          KG +FFR+FG N+
                          +S LG+ P++ +LIG
                                             M DAY +G ID + + NKF+NTM+
Sbjct: 121 KGAAFFRNFGGNVVAAISHLGEEPSINDLIGSVKVMLDAYLDGRIDRLSVVSNKFINTMT 180
Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
          Q+P V+QL+PL + D L
                                   WDYLYEP+ K LLD L+VRY+ESQ+YQAVV+N A+
Sbjct: 181 QQPTVEQLIPLVATPDQGLKHH---WDYLYEPDAKELLDGLMVRYVESQVYQAVVENNAA 237
Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
          EQAARM+AMK ATDNAG+LI+DL+L+YNKARQA+IT E++EIV GAAA+
Sbjct: 238 EQAARMIAMKNATDNAGDLISDLQLIYNKARQAAITQEISEIVGGAAAV 286
tr Q83AF6 ATP synthase, F1 gamma subunit [ATPG] [Coxiella burnetii] 289 AA
                                                                     aliqn
Score = 338 bits (868), Expect = 4e-92
Identities = 169/291 (58%), Positives = 223/291 (76%), Gaps = 5/291 (1%)
Query: 1
          MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
          M+ A+EI+TKIAS+++TQKIT+AME+VA SKMRK QDRMA SRPY+ IR VISHV+ +
Sbjct: 1
          MSKAREIRTKIASIKNTQKITRAMELVAASKMRKAQDRMAMSRPYASKIRKVISHVAASH 60
Query: 61 IGYKHPFLVERE-VKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIG 119
```

Y HP+L +RE +K++G ++++TDRG+CGGLNVNLF+T + +K W+ NI DL +IG

Sbjct: 61 AEYPHPYLQQRENIKRVGYIIVTTDRGLCGGLNVNLFRTAIADMKKWQADNIGMDLCVIG 120

Query: 120 SKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTM 179

LGD P ++++IG+ M D Y

KG +FFR +G N+

+IDA+YIA N+FVNTM

```
Sbjct: 121 RKGEAFFRRYGGNVLAVADHLGDAPEVQDIIGIVKVMLDQYDKQQIDAIYIATNEFVNTM 180
```

Query: 180 SQKPVVQQLVPLPESKDDHLNERQQTWDYLYEP-EPKVLLDSLLVRYLESQIYQAVVDNV 238

K D WDY+YEP E K LL+ LLVRY+ESQ+YQAV++N+ QKP+V+QL+PL

Sbjct: 181 VQKPLVRQLLPL---KTDEEEVEGGYWDYIYEPDESKDLLEMLLVRYIESQVYQAVIENI 237

Ouery: 239 ASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289

A EO+ARMVAMK AT+NAG LI++LRL+YNKAROA IT E+ EIVAGAAA+

Sbjct: 238 ACEQSARMVAMKNATENAGQLIDELRLIYNKARQAGITREIAEIVAGAAAV 288

tr <u>Q82XP9</u> ATP synthase gamma subunit (EC 3.6.3.14) [ATPG] [Nitrosomonas 294 AA europaea]

align

Score = 337 bits (865), Expect = 1e-91 Identities = 159/294 (54%), Positives = 222/294 (75%), Gaps = 5/294 (1%)

MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60 Query: 1 M ++EI+ KI SV++TQKIT+AMEMVA SKMRK QDRM +RPY E IRNV +H+S AS

Sbjct: 1 MPSSREIRNKIKSVKNTQKITRAMEMVAASKMRKAQDRMKKARPYGEKIRNVAAHMSNAS 60

IGYKHPFLVERE-VKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIG 119 Query: 61 + Y+HPFL+ R+ VK++GI+V+++D+G+CGGLN N+ + LN+I+ W+ +

Sbjct: 61 VEYRHPFLISRDSVKRVGIIVVTSDKGLCGGLNTNVLRRALNEIRTWETEGNHVDACCIG 120

Query: 120 SKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTM 179

G + Q++GLGD P +E LIG

+ DAY G++D VYI YN+F+NTM Sbjct: 121 NKGLGFMSRLGTQVISQVTGLGDAPNMERLIGAVKVVLDAYTEGQLDRVYIFYNRFINTM 180

Query: 180 SQKPVVQQLVPLPE----SKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVV 235

Q PV++QL+PL + S+D+ WDY+YEPE K ++D ++VRY+E+ +YQAV

Sbjct: 181 KQMPVMEQLLPLTDDRISSEDGEARPTRAPWDYIYEPEAKPVIDDIMVRYIEALVYQAVA 240

Query: 236 DNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289

+N+ASEQ+ARMVAMKAA+DNAGNLI++L L+YNK+RQA+IT EL+EIV GAAA+

Sbjct: 241 ENMASEQSARMVAMKAASDNAGNLIDELTLIYNKSRQAAITKELSEIVGGAAAV 294

tr Q8XU75 Probable ATP synthase gamma chain protein (EC 3.6.1.34) [ATPG] 291 AA [Ralstonia solanacearum (Pseudomonas solanacearum)]

aliqn

Score = 331 bits (848), Expect = 9e-90 Identities = 158/291 (54%), Positives = 223/291 (76%), Gaps = 2/291 (0%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60 MAG KEI+TKI SVQ+T+KITKAMEMVA SKMR+ Q+RM ++RPY+E IRNV +H+++A+

Sbjct: 1 MAGTKEIRTKIKSVQNTRKITKAMEMVAASKMRRAQERMRSARPYAEKIRNVAAHMAQAN 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120 Y+HPF+V+R+VK+ G++V++TD+G+CGGLN N+ + NQ+++ + + + +

Sbjct: 61 PEYQHPFMVKRDVKRAGLIVVTTDKGLCGGLNTNVLRAVTNQLRDLQNKGVESQATAIGS 120

Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180

```
G + + LGDTP LE+LIG
                                               DA+ GEIDAVY+AY +F+NTM
Sbjct: 121 KGMQFLGRIGAKVVSNVVHLGDTPHLEKLIGAIKVQLDAFTAGEIDAVYLAYTRFINTMR 180
Query: 181 QKPVVQQLVPLPESKDDHLNERQQ--TWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNV 238
                       K +Q +WDY+YEP+ + ++D LL+RY+E+ +YQAV +N+
           Q+PVV+QL+PL
Sbjct: 181 QEPVVEQLLPLTADKLTQTAAEKQAYSWDYIYEPDAQTVVDELLIRYVEALVYQAVAENM 240
Ouery: 239 ASEOAARMVAMKAATDNAGNLINDLRLVYNKAROASITNELNEIVAGAAAI 289
          ASEQ+ARMVAMKAA+DNA N+I +L+LVYNK RQA+IT EL+EIV GAAA+
Sbjct: 241 ASEQSARMVAMKAASDNAKNVIGELQLVYNKTRQAAITKELSEIVGGAAAV 291
tr Q8PCZ6 ATP synthase gamma chain [ATPG] [Xanthomonas campestris (pv. 287 AA
           campestris)]
                                                                        aliqn
 Score = 323 bits (827), Expect = 2e-87
 Identities = 155/290 (53%), Positives = 220/290 (75%), Gaps = 4/290 (1%)
Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
          MAG +EIKTKI SVQ+T+K+T+A+EMV+ SK+RK Q+RM SRPY++ ++ VI H+++AS
Sbict: 1
          MAGGREIKTKIKSVQNTRKVTRALEMVSASKIRKAQERMKTSRPYAQAMKQVIGHLAQAS 60
Query: 61 IGYKHPFLVERE-VKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIG 119
            Y+HPFLVERE VK++G +VIS+DRG+ GGLN NLF+ L +++ W+++
Sbjct: 61 TDYQHPFLVEREQVKRVGYIVISSDRGLAGGLNNNLFRKMLGEVRPWQDKGAEIDVVTIG 120
Query: 120 SKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTM 179
                      N+ G ++ LGD+P +E+L+GV
                                             M DA+ G++D VY+ YN+FVNTM
Sbjct: 121 QKASAFFRRIKVNMVGSVTHLGDSPHIEQLVGVIKVMLDAFTEGKVDRVYLVYNRFVNTM 180
Query: 180 SQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVA 239
           +QK
                +QL+PLP ++
                                    WDYLYEP+
                                              +L+ ++ RY+ES +YQAV++NVA
Sbjct: 181 TQKASFEQLLPLPAAEH---KVAHHDWDYLYEPDAATVLEHVMTRYIESLVYQAVLENVA 237
Query: 240 SEQAARMVAMKAATDNAGNLINDLRLVYNKAROASITNELNEIVAGAAAI 289
          SE AARMVAMKAA+DNA +I L+LVYNKARQA+IT E++EIV+GAAA+
Sbjct: 238 SEHAARMVAMKAASDNANKMIGTLQLVYNKARQAAITQEISEIVSGAAAV 287
sp 051873
              ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Buchnera
                                                                          291
   ATPG BUCAP aphidicola
                                                                          AΑ
               (subsp. Schizaphis graminum)]
                                                                          align
Score = 322 bits (826), Expect = 3e-87
Identities = 162/289 (56%), Positives = 218/289 (75%), Gaps = 1/289 (0%)
Query: 1
          MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
              KEIK +I SV +T+KITKAMEMVA SKMRKT++RM
                                                    RPYSE I+ VI HV + S
Sbjct: 1
          MASKKEIKDQIISVTNTKKITKAMEMVAVSKMRKTEERMRLGRPYSEIIKKVIHHVLQGS 60
Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
          + YKH +L +R K+IGI+++STDRG+CG LN NLFK L +I+N+ + NI DL L G
Sbjct: 61 LEYKHSYLEKRNDKRIGIIIVSTDRGLCGSLNTNLFKQVLFKIQNFAKINIPCDLILFGL 120
```

```
Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
           K +S F+ +G +I
                          ++ LG+TP L +LIG
                                              + + Y+N +ID ++IAYNKF N +S
Sbjct: 121 KSLSVFKLYGSSIISSVTNLGETPDLSKLIGSIKIILEKYQNNQIDRLFIAYNKFHNKLS 180
Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
           Q P + QL+PL
                        K+
                              N++ + WDYLYEPE K++LD+L RY+ESQIYO++++N+AS
Sbjct: 181 QYPKISQLLPLYNEKNIFSNKKIK-WDYLYEPESKLILDTLFDRYIESQIYOSLLENIAS 239
Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
           EQAARMVAMK ATDN+GN I +L+L+YNK RQA+IT EL EIVAGA+A+
Sbjct: 240 EQAARMVAMKTATDNSGNRIKELQLIYNKVRQANITQELTEIVAGASAV 288
               ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Buchnera
sp P57123
                                                                           290
   ATPG BUCAI aphidicola
                                                                           AA
               (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                           align
               symbiotic bacterium)]
 Score = 322 bits (826), Expect = 3e-87
 Identities = 161/289 (55%), Positives = 212/289 (72%), Gaps = 2/289 (0%)
Query: 1
           MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
               KEIK KI SV +T+KITKAMEMVA SKMRKT++RM + RPYS+ TR VI HV++ +
          MTSTKEIKNKIVSVTNTKKITKAMEMVAVSKMRKTEERMRSGRPYSDIIRKVIDHVTQGN 60
Sbjct: 1
Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNOIKNWKEONISTDLGLIGS 120
           + YKH +L ER+ +IG+++ISTDRG+CGGLN NLFK L +I+N+ + NI DL L G
Sbjct: 61 LEYKHSYLEERKTNRIGMIIISTDRGLCGGLNTNLFKQVLFKIQNFAKVNIPCDLILFGL 120
Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
           K +S F+ G NI + + LG+ P LEELI
                                             +
                                                  Y+
                                                      ID ++IAYNKF N MS
Sbjct: 121 KSLSVFKLCGSNILAKATNLGENPKLEELINSVGIILQEYQCKRIDKIFIAYNKFHNKMS 180
Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
           Q P + QL LP SK + + WDYLYEPE K++LD+L RY+ESQ+YQ++++N+AS
Sbjct: 181 QYPTITQL--LPFSKKNDQDASNNNWDYLYEPESKLILDTLFNRYIESOVYOSILENIAS 238
Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
           E AARM+AMK ATDN+GN I +L+LVYNK RQA+IT ELNEIV+GA+A+
Sbjct: 239 EHAARMIAMKTATDNSGNRIKELQLVYNKVRQANITQELNEIVSGASAV 287
tr Q8PGG6 ATP synthase gamma chain [ATPG] [Xanthomonas axonopodis (pv. 287 AA
           citri)]
                                                                        align
Score = 318 bits (816), Expect = 5e-86
Identities = 154/290 (53%), Positives = 219/290 (75%), Gaps = 4/290 (1%)
Query: 1
          MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
          MAG +EIKTKI SVQ+T+K+T+A+EMV+ SK+RK O+RM SRPY++ ++ VI H+++AS
Sbjct: 1
          MAGGREIKTKIKSVQNTRKVTRALEMVSASKIRKAQERMKTSRPYAQAMKQVIGHLAQAS 60
Query: 61 IGYKHPFLVERE-VKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIG 119
             ++HPFL+ERE VK++G +VIS+DRG+ GGLN NLF+ L +++ W+++
```

Sbjct: 1

Sbjct: 61

FFR

```
Sbjct: 61 TDFQHPFLIEREQVKRVGYIVISSDRGLAGGLNNNLFRKMLGEVRPWQDKGAEIDVVTIG 120
```

Query: 120 SKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTM 179

N+ G ++ LGD+P +E+LIGV M DA+ G++D VY+ YN+FVNTM +FFR

Sbjct: 121 QKASAFFRRVKVNMVGSVTHLGDSPQVEQLIGVIKVMIDAFIEGKVDRVYLVYNRFVNTM 180

Query: 180 SQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVA 239

WDYLYEP+ +L+ ++ RY+ES +YOAV++NVA OL+PLP ++ +0K

Sbjct: 181 TQKASFDQLLPLPAAEH---KVAHHDWDYLYEPDAASVLEHVMTRYIESLVYQAVLENVA 237

Query: 240 SEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289

SE AARMVAMKAA+DNA +I L+LVYNKARQA+IT E++EIV+GAAA+

Sbjct: 238 SEHAARMVAMKAASDNANKMIGTLQLVYNKARQAAITQEISEIVSGAAAV 287

tr Q87E89 ATP synthase gamma chain [ATPG] [Xylella fastidiosa (strain 287 AA Temecula1 / ATCC 700964)]

align

Score = 305 bits (781), Expect = 5e-82 Identities = 150/290 (51%), Positives = 209/290 (71%), Gaps = 4/290 (1%)

MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60 Query: 1 +EIK+KI SVQ+T+K+T+A+EMV+ SK+RK Q++M SRPY++ ++ +I H+++A+

MASGREIKSKIKSVQNTRKVTRALEMVSASKIRKAQEQMKISRPYAQAMKQMIGHLAQAN 60

IGYKHPFLV-EREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIG 119 Query: 61

Y HPFL+ ++VK+IG +VIS+DRG+ GGLN NLF+ L ++ W++ TEYLHPFLIAHKQVKRIGYIVISSDRGLAGGLNNNLFRKMLGEMHQWQDNGAEVDIVTIG 120

Query: 120 SKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTM 179

NI G ++ LGDTP LE+LIGV M DAY ++D VY+ YN F+NTM Sbjct: 121 QKASVFFRRIKVNILGSVTHLGDTPRLEQLIGVIKVMLDAYTEEKLDRVYLVYNHFINTM 180

Query: 180 SQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVA 239

OK OL+PL +KD WDYLYEP+ +L+ ++ RY+ES +YOA+++N+A

Sbjct: 181 VQKASFDQLLPLLAAKD---KVAHHDWDYLYEPDAATVLEHVMTRYIESLVYQAMLENIA 237

Query: 240 SEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289

SE AARMVAMKAA+DNA LI L+LVYNKAROA+IT E++EIV GAAA+

Sbjct: 238 SEHAARMVAMKAASDNANKLIGTLQLVYNKARQAAITQEISEIVGGAAAV 287

ATP synthase, gamma chain [XF1144] [Xylella 287 AA tr **Q9PE84** fastidiosa] align

Score = 305 bits (781), Expect = 5e-82 Identities = 149/290 (51%), Positives = 211/290 (72%), Gaps = 4/290 (1%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60 +EIK+KI SVQ+T+K+T+A+EMV+ SK+RK Q++M SRPY++ ++ + H+++A+

Sbjct: 1 MASGREIKSKIKSVQNTRKVTRALEMVSASKIRKAQEQMKISRPYAQAMKQMTGHLAQAN 60

IGYKHPFLV-EREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIG 119 Query: 61 Y HPFL+ ++VK+IG +VIS+DRG+ GGLN NLF+ L +++ W+++ D+ IG·

```
Sbjct: 61 TDYLHPFLIAHKQVKRIGYIVISSDRGLAGGLNNNLFRKMLGEMRQWQDKGAEVDIVTIG 120
Query: 120 SKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTM 179
                FFR
                      NI G ++ LGDTP LE+LIGV
                                              M DAY
                                                      ++D VY+ YN+F+NTM
Sbjct: 121 QKASVFFRRIKVNILGSVTHLGDTPRLEQLIGVIKVMLDAYTEEKLDRVYLVYNRFINTM 180
Query: 180 SQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVA 239
            QΚ
                  QL+PL +KD
                                    WDYLYEP+
                                               +L+ ++ RY+ES +YQA+++N+A
Sbjct: 181 VQKASFDQLLPLLAAKD---KVAHHDWDYLYEPDAATVLEHVMRRYIESLVYQAMLENIA 237
Query: 240 SEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
           SE AARMVAMKAA+DNA LI L+LVYNKARQA+IT E++EIV GAAA+
Sbjct: 238 SEHAARMVAMKAASDNANKLIGTLQLVYNKARQAAITQEISEIVGGAAAV 287
tr Q7VU45 ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Bordetella 301 AA
          pertussis]
                                                                     align
 Score = 304 bits (779), Expect = 9e-82
 Identities = 149/301 (49%), Positives = 208/301 (68%), Gaps = 12/301 (3%)
Query: 1
          MAGAKEIKTKIASVOSTOKITKAMEMVATSKMRKTODRMAASRPYSETIRNVISHVSKAS 60
          M G KEI+TKI SVQ+T+KITKAMEMVA SKMRK Q+RM A RPY+ +R + +H+ +A+
Sbjct: 1
          MPGIKEIRTKIKSVQNTRKITKAMEMVAASKMRKAQERMRAGRPYATKVREIAAHLMQAN 60
Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
             Y HP+LVEREVK +G+++++TD+G+CGGLN N+ + TL+++K +++++1
Sbjct: 61 PEYSHPYLVEREVKAVGVVLVTTDKGLCGGLNTNISRVTLSKLKEFEQRSIKVQATAFGN 120
Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
                             LGD P L+ L+G
                   G + Q
                                               D Y G IDA+Y+A +FVNTM
Sbjct: 121 KGLGLLTRIGAKLVSQEVQLGDKPDLDRLLGAIKVQLDDYLEGRIDALYVATTRFVNTMK 180
Query: 181 QKPVVQQLVPLPESKDDHLNERQQT------WDYLYEPEPKVLLDSLLVRYLES 228
                                 +T
           Q+PV +L+PL
                         DD
                                               WDY+YEP+ K ++D LL RY+E
Sbjct: 181 QEPVFLRLLPLSNGLDDPFQSGVETLAKTAEIKSDYSWDYIYEPDAKSVIDDLLQRYVEG 240
Query: 229 QIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAA 288
            +YQAV +N+ASEQ+ARMVAMK+A+DNA +I DL+LVYNK RQA+IT E++EIV GAAA
Sbjct: 241 LLYQAVAENMASEQSARMVAMKSASDNAKKVIGDLQLVYNKTRQAAITKEISEIVGGAAA 300
Query: 289 I 289
Sbjct: 301 V 301
tr Q7WEM8 ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Bordetella 301 AA
          bronchiseptica (Alcaligenes bronchisepticus)]
                                                                     align
 Score = 304 bits (778), Expect = 1e-81
Identities = 149/301 (49%), Positives = 208/301 (68%), Gaps = 12/301 (3%)
```

Query: 1 MAGAKEIKTKIASVOSTOKITKAMEMVATSKMRKTODRMAASRPYSETIRNVISHVSKAS 60

- M G KEI+TKI SVQ+T+KITKAMEMVA SKMRK Q+RM A RPY+ +R + +H+ +A+ MPGIKEIRTKIKSVQNTRKITKAMEMVAASKMRKAQERMRAGRPYATKVREIAAHLMQAN 60 Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120 Y HP+LVEREVK +G+++++TD+G+CGGLN N+ + TL+++K +++++I Sbjct: 61 PEYSHPYLVEREVKAVGVVLVTTDKGLCGGLNTNISRVTLSKLKEFEORSIKVOATAFGN 120 Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180 G + Q LGD P L+ L+G D Y G IDA+Y+A Sbjct: 121 KGLGLLTRIGAKLVSQEVQLGDKPDLDRLLGAIKVQLDDYLEGRIDALYVATTRFVNTMR 180 Query: 181 QKPVVQQLVPLPESKDDHLNERQQT-------WDYLYEPEPKVLLDSLLVRYLES 228 Q+PV +L+PL +TWDY+YEP+ K ++D LL RY+E Sbjct: 181 QEPVFLRLLPLSNGLDDPFQSGVETLAKTAEIKSDYSWDYIYEPDAKSVIDDLLQRYVEG 240 Query: 229 QIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAA 288 +YQAV +N+ASEQ+ARMVAMK+A+DNA +I DL+LVYNK RQA+IT E++EIV GAAA Sbjct: 241 LLYQAVAENMASEQSARMVAMKSASDNAKKVIGDLQLVYNKTRQAAITKEISEIVGGAAA 300 Query: 289 I 289 Sbjct: 301 V 301
- tr Q7W3A9 ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Bordetella 301 AA parapertussis]

align

```
Score = 303 bits (776), Expect = 2e-81
 Identities = 149/301 (49%), Positives = 208/301 (68%), Gaps = 12/301 (3%)
Query: 1
          MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
          M G KEI+TKI SVQ+T+KITKAMEMVA SKMRK Q+RM A RPY+
Sbjct: 1
          MPGIKEIRTKIKSVQNTRKITKAMEMVAASKMRKAQERMRAGRPYATKVREIAAHLMQAN 60
          IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
Query: 61
             Y HP+LVEREVK +G+++++TD+G+CGGLN N+ + TL+++K +++++1
Sbjct: 61 PEYGHPYLVEREVKAVGVVLVTTDKGLCGGLNTNISRVTLSKLKEFEQRSIKVQATAFGN 120
Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
                   G + Q LGD P L + L + G
                                               D Y G IDA+Y+A +FVNTM
Sbjct: 121 KGLGLLTRIGAKLVSQEVQLGDKPDLDRLLGAIKVQLDDYLEGRIDALYVATTRFVNTMR 180
Query: 181 QKPVVQQLVPLPESKDDHLNERQQT------WDYLYEPEPKVLLDSLLVRYLES 228
           Q+PV +L+PL
                         DD
                                 +T
                                               WDY+YEP+ K ++D LL RY+E
Sbjct: 181 QEPVFLRLLPLSNGLDDPFQSGVETLAKTAEIKSDYSWDYIYEPDAKSVIDDLLQRYVEG 240
Query: 229 QIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAA 288
            +YQAV +N+ASEQ+ARMVAMK+A+DNA +I DL+LVYNK RQA+IT E++EIV GAAA
Sbjct: 241 LLYQAVAENMASEQSARMVAMKSASDNAKKVIGDLQLVYNKTRQAAITKEISEIVGGAAA 300
Query: 289 I 289
Sbjct: 301 V 301
```

tr Q7VQV7 ATP synthase gamma subunit (EC 3.6.3.14) [ATPG] [Candidatus 288 AA Blochmannia floridanus]

align

298

align

AA

Score = 302 bits (774), Expect = 3e-81
Identities = 147/291 (50%), Positives = 209/291 (71%), Gaps = 5/291 (1%)

- Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60 M+ KE++ KI S+++ QK++KAMEM+A SKM+K Q M S+PY++ IR VI H+S
- Sbjct: 1 MSSIKEVREKIESIRNIQKLSKAMEMIAASKMKKAQRLMLVSQPYTKAIRKVIDHISLGK 60
- Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
 + Y+H +L+ REV+ +G VIS+DRG+ GGLNVN+F+ LN I W + N++ L +IGS
- Sbjct: 61 LEYRHVYLMNREVRSVGYWVISSDRGLAGGLNVNVFRMLLNDISRWNKLNVTIKLAIIGS 120
- Query: 121 KGISFFRSFGFN-IKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTM 179

 K ISFF N I +SG+GD P + +LIG+ TM Y NG++D +Y+ YNKF+NT+
- Sbjct: 121 KAISFFNCIDPNMIVSYVSGIGDVPKMSQLIGLVGTMLQLYCNGQVDRLYLIYNKFINTL 180
- Query: 180 SQKPVVQQLVPL-PESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNV 238 SQ P + Q++P+ ES + + + WDYLYEP+ KVLLD+LL RY+ESO+YO VV+N+
- Sbjct: 181 SQVPKIIQILPIFSESNNTCVTKH---WDYLYEPDSKVLLDTLLNRYIESQVYQGVVENL 237
- Query: 239 ASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289 ASEQ+ARM+AMK A+DN +I DLR+ YNK RO+ IT EL EI++G++ I
- Sbjct: 238 ASEQSARMIAMKTASDNGETIIKDLRVFYNKLRQSKITQELAEIISGSSVI 288

sp P41169 ATP synthase gamma chain (EC 3.6.3.14) [ATPG] ATPG_THIFE [Thiobacillus ferrooxidans]

Score = 301 bits (771), Expect = 8e-81 Identities = 144/287 (50%), Positives = 213/287 (74%), Gaps = 1/287 (0%)

- Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60 MA AKEI+ +I SV++T+KIT+AMEMVA SKMR+ Q+RM A+RP +E IR V+ H+++A
- Sbjct: 1 MANAKEIRGQIKSVKNTRKITRAMEMVAASKMRRAQERMRAARPCAEKIREVLGHLAQAH 60
- Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
 Y+HP + R VKK G LV++TDRG+CGGLNVN+ + + +++ E+ +++L ++G+
- Sbjct: 61 PEYEHPLMQVRPVKKAGFLVVTTDRGLCGGLNVNVLRNVVQKMRELHEEGVESNLAVVGN 120
- Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180 KG+ F R G ++ ++GLGD+P L ++IG M DAY GE+D VY+ ++FVNTM
- Sbjct: 121 KGLGFLRRHGAHLVADVNGLGDSPHLGDMIGPIRAMADAYAKGEVDVVYLVSSRFVNTML 180
- Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
- Sbjct: 181 QRATVEQLLPV-EKPTASAEQRAELWDYIYEPEARPVLDRLMQRYVESVVYQAVIEHLAC 239

Q+V+QL+P+E +R + WDY+YEPE + +LD L+ RY+ES +YQAV++++A

- Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAA 287
 - EQ+ARMVAMK+A+DNA +++DL+L YNKARQA+IT E+ EI AGAA
- Sbjct: 240 EQSARMVAMKSASDNAKRMVDDLQLAYNKARQAAITQEIAEISAGAA 286

```
Score = 300 bits (768), Expect = 2e-80
 Identities = 149/277 (53%), Positives = 205/277 (73%), Gaps = 3/277 (1%)
Query: 14 VQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVERE- 72
          +O+TOKIT+AM+MV+TSKMRKTQ+RM A+RPY+E +R V++H+++A+
          MQNTQKITRAMQMVSTSKMRKTQERMRAARPYAEKVRTVMAHLAQANAELGHPLLARRET 60
Sbjct: 1
Query: 73 VKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFN 132
           +K+ GI+++S+D+G+CGGLNVN FK
                                       ++K ++Q I D+ +G KG++ +
Sbjct: 61 IKRAGIILVSSDKGLCGGLNVNSFKRFFGKVKELQDQGIEVDVCCLGQKGLAAAQRARLN 120
Query: 133 IKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMSQKPVVQQLVPLP 192
                 LGD P +E+LIG
                                 +F Y GE+DAVYI Y+ FVNTM Q+P ++QL+PL
Sbjct: 121 VVASAVHLGDMPKMEKLIGPLTVLFRQYAEGELDAVYIVYSSFVNTMKQEPALEQLLPL- 179
Query: 193 ESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVASEQAARMVAMKAA 252
                      +WDYLYEP+ L++ L+ RYLES +YQA+ +N+ASEQAARMVAMKAA
                + E
Sbjct: 180 -TPHHMVVEHSHSWDYLYEPDAPTLMEFLVRRYLESVVYQALAENMASEQAARMVAMKAA 238
Query: 253 TDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
           TDNAGN I LRLVYNKARQA+IT EL+EIVAGAAA+
```

tr <u>Q83U82</u> ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Haemophilus 150 AA influenzae]

align

tr <u>Q83V88</u> ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Haemophilus 150 AA influenzae]

align

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Score = 296 bits (759), Expect = 2e-79
Identities = 149/150 (99%), Positives = 150/150 (99%)
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Sbjct: 239 TDNAGNTIKQLRLVYNKARQAAITTELSEIVAGAAAV 275

Score = 297 bits (760), Expect = 1e-79

Query: 22 KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI 81

KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI Sbjct: 1 KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI 60 Query: 82 STDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG 141 STDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGOLSGLG Sbjct: 61 STDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG 120 Query: 142 DTPALEELIGVANTMFDAYRNGEIDAVYIA 171 DTPALEELIGVANTMFDAYRNGEIDA+YIA Sbjct: 121 DTPALEELIGVANTMFDAYRNGEIDAIYIA 150 tr <u>Q83V83</u> ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Haemophilus 150 AA influenzae] align Score = 296 bits (758), Expect = 2e-79 Identities = 148/150 (98%), Positives = 150/150 (99%) Query: 22 KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI 81 KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFL+EREVKKIGILVI Sbjct: 1 KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLIEREVKKIGILVI 60 Query: 82 STDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG 141 ${\tt STDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG}$ Sbjct: 61 STDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG 120 Query: 142 DTPALEELIGVANTMFDAYRNGEIDAVYIA 171 DTPALEELIGVANTMFDAYRNGEIDA+YIA Sbjct: 121 DTPALEELIGVANTMFDAYRNGEIDAIYIA 150 tr <u>Q83V86</u> ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Haemophilus 150 AA influenzae] aliqn Score = 295 bits (756), Expect = 4e-79Identities = 148/150 (98%), Positives = 150/150 (99%) Query: 22 KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI 81

- KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI
- Sbjct: 1 KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI 60
- Query: 82 STDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG 141 STDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGOLSGLG
- Sbjct: 61 STDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG 120
- Query: 142 DTPALEELIGVANTMFDAYRNGEIDAVYIA 171

DTPAL+ELIGVANTMFDAYRNGEIDA+YIA

Sbjct: 121 DTPALQELIGVANTMFDAYRNGEIDAIYIA 150

tr Q9RQ80 Gamma subunit of membrane-bound ATP synthase [ATPG] [Buchnera 290 AA

aphidicola]

align

Score = 295 bits (756), Expect = 4e-79
Identities = 145/289 (50%), Positives = 214/289 (73%), Gaps = 2/289 (0%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60 MA KEIKT+I SV +T+KITKAMEMVA SKMRKT++RM++ RPYSE IR VI+HV++

Sbjct: 1 MASIKEIKTQITSVVNTKKITKAMEMVAISKMRKTEERMSSGRPYSEIIRKVINHVAQGH 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
+ YKH +L R++K+IG++++S+DRG+CG LN NLF+ L +I+N+ ++NI DL L G

Sbjct: 61 LEYKHSYLETRKIKRIGLIIVSSDRGLCGSLNSNLFRKVLFKIQNFTQKNIPCDLILFGL 120

Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180 K + F+ NI +++ LG+ P + ++I + + Y+ ID ++IAYN+F N MS

Sbjct: 121 KSLPVFKLCENNILSKITHLGEHPNILKVINGIDVLLKKYQIKRIDKIFIAYNEFHNKMS 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240

Q P + QL+PL K + ++ ++ WDYLYE E K+++DSL RY+ESQ+YQ++++N+AS Sbjct: 181 QYPKIIQLLPLSRIKSETISTKR--WDYLYESESKLIIDSLFKRYIESQVYQSILENIAS 238

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
E AARM+AMK AT+N+ I +L+L+YNK RQA+IT EL EI+AGA+A+

Sbjct: 239 EHAARMMAMKTATENSTERIKELKLLYNKVRQATITQELTEIIAGASAV 287

tr Q9JW71 ATP synthase gamma chain (EC 3.6.1.34) [ATPG] 291 AA [Neisseria align meningitidis (serogroup A)]

Score = 295 bits (755), Expect = 5e-79 Identities = 150/291 (51%), Positives = 211/291 (71%), Gaps = 2/291 (0%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60 MA KEI TKI SVQ+TQKITKAM+MV+TSKMRKTQ+RM +RPY+E +R V+SH+++ +

Sbjct: 1 MAVGKEILTKIRSVQNTQKITKAMQMVSTSKMRKTQERMRLARPYAEKVRMVMSHLAQTN 60

Query: 61 IGYKHPFLVE-REVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIG 119
+ P L RE++++G ++I++D+G+CGGLN N+ K L Q++ ++ Q I ++ +G

Sbjct: 61 TDHGIPLLESHREIRRVGFILITSDKGLCGGLNANVLKKFLAQVQEYQNQGIEEEIVCLG 120

Query: 120 SKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTM 179 SKG+ +S G N+ LGDTP +E L+G +F Y EID +++ Y+ FVNTM

Sbjct: 121 SKGLMACQSIGLNVVASAVNLGDTPKMEMLLGPLTELFQRYEKHEIDRIHLVYSGFVNTM 180

Query: 180 SQKPVVQQLVPLPESK-DDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNV 238

Q+P ++ L+P+ E+ D + +W+Y YEP +L+ L+ RYLES +YQA+ DN+

Sbjct: 181 RQEPRMEVLLPIGENVIGDSAPKSPFSWEYRYEPTALAVLEYLVRRYLESVVYQALSDNM 240

Query: 239 ASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289 ASEQAARMVAMKAATDNAGN I +LRLVYNK+RQA+IT.EL+EIVAGAAA+

Sbjct: 241 ASEQAARMVAMKAATDNAGNAIKELRLVYNKSRQAAITTELSEIVAGAAAV 291

tr Q83U83 ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Haemophilus 150 AA influenzae] align Score = 295 bits (755), Expect = 5e-79 Identities = 148/150 (98%), Positives = 149/150 (98%) Query: 22 KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI 81 KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI Sbjct: 1 KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI 60 Query: 82 STDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG 141 STDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG Sbjct: 61 STDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG 120 Query: 142 DTPALEELIGVANTMFDAYRNGEIDAVYIA 171 DTP LEELIGVANTMFDAYRNGEIDA+YIA Sbjct: 121 DTPVLEELIGVANTMFDAYRNGEIDAIYIA 150 tr Q9JXQ1 ATP synthase F1, gamma subunit [NMB1935] [Neisseria 291 meningitidis AΑ (serogroup B)] align Score = 295 bits (754), Expect = 7e-79 Identities = 150/291 (51%), Positives = 210/291 (71%), Gaps = 2/291 (0%) Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60 MA KEI TKI SVQ+TQKITKAM+MV+TSKMRKTQ+RM +RPY+E +R V+SH+++ + Sbjct: 1 ${\tt MAVGKEILTKIRSVQNTQKITKAMQMVSTSKMRKTQERMRLARPYAEKVRMVMSHLAQTN~60}$ Query: 61 IGYKHPFLVE-REVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIG 119 RE++++G ++I++D+G+CGGLN N+ K L Q++ ++ Q I ++ Sbjct: 61 TDHGIPLLESHREIRRVGFILITSDKGLCGGLNANVLKKFLAQVQEYRNQGIEEEIVCFG 120 Query: 120 SKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTM 179 SKG+ +S G N+ LGDTP +E L+G +F Y EID +++ Y+ FVNTM Sbjct: 121 SKGLMACQSIGLNVVASAVNLGDTPKMEMLLGPLTELFQRYEKHEIDRIHLVYSGFVNTM 180 Query: 180 SQKPVVQQLVPLPESK-DDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNV 238 Q+P ++ L+P+ E+ D + +W+Y YEP +L+ L+ RYLES +YQA+ DN+ Sbjct: 181 RQEPRMEVLLPIGENVIGDSAPKSPFSWEYRYEPTALAVLEYLVRRYLESVVYOALSDNM 240 Query: 239 ASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289 ASEQAARMVAMKAATDNAGN I +LRLVYNK+RQA+IT EL+EIVAGAAA+ Sbjct: 241 ASEQAARMVAMKAATDNAGNAIKELRLVYNKSRQAAITTELSEIVAGAAAV 291

tr Q83V85 ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Haemophilus 150 AA influenzae]

align

Score = 294 bits (753), Expect = 9e-79 Identities = 148/150 (98%), Positives = 149/150 (98%)

- KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI 81 KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI Sbjct: 1 KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI 60 Query: 82 STDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG 141 STDRGMCGGLNVNLFKT LNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGOLSGLG STDRGMCGGLNVNLFKTILNOIKNWKEONISTDLGLIGSKGISFFRSFGFNIKGOLSGLG 120 Sbjct: 61 Query: 142 DTPALEELIGVANTMFDAYRNGEIDAVYIA 171 DTPALEELIGVANTMFDAYRNGEIDA+YIA Sbjct: 121 DTPALEELIGVANTMFDAYRNGEIDAIYIA 150 tr Q83V87 ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Haemophilus 150 AA influenzae] aliqn Score = 294 bits (752), Expect = 1e-78 Identities = 149/150 (99%), Positives = 149/150 (99%) Query: 22 KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI 81 KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVE EVKKIGILVI Sbjct: 1 KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVECEVKKIGILVI 60 STDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG 141 STDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG Sbjct: 61 STDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG 120 Query: 142 DTPALEELIGVANTMFDAYRNGEIDAVYIA 171 DTPALEELIGVANTMFDAYRNGEIDAVYIA Sbjct: 121 DTPALEELIGVANTMFDAYRNGEIDAVYIA 150 tr Q83UA6 ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Haemophilus 150 AA influenzae] aliqn Score = 293 bits (750), Expect = 2e-78 Identities = 147/150 (98%), Positives = 149/150 (99%)
- Query: 22 KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI 81
 KAMEMVATSK+RKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI
 Sbjct: 1 KAMEMVATSKLRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI 60
- Query: 82 STDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG 141 STDRGMCGGLNVNLFKT LNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG
- Sbjct: 61 STDRGMCGGLNVNLFKTILNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG 120
- Query: 142 DTPALEELIGVANTMFDAYRNGEIDAVYIA 171

DTPALEELIGVANTMFDAYRNGEIDA+YIA

Sbjct: 121 DTPALEELIGVANTMFDAYRNGEIDAIYIA 150

tr <u>Q83V84</u> ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Haemophilus 150 AA influenzae]

align

Score = 293 bits (750), Expect = 2e-78
Identities = 147/150 (98%), Positives = 149/150 (99%)

- Query: 22 KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI 81 KAMEMVATSKMRKTQDRMAASRPYSETIR+VISHVSKASIGYKHPFLVEREVKKIGILVI
- Sbjct: 1 KAMEMVATSKMRKTQDRMAASRPYSETIRSVISHVSKASIGYKHPFLVEREVKKIGILVI 60
- Query: 82 STDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG 141 STDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG
- Sbjct: 61 STDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG 120
- Query: 142 DTPALEELIGVANTMFDAYRNGEIDAVYIA 171
 DTP LEELIGVANTMFDAYRNGEIDA+YIA
- Sbjct: 121 DTPVLEELIGVANTMFDAYRNGEIDAIYIA 150

tr <u>Q83V89</u> ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Haemophilus 150 AA influenzae]

aliqn

Score = 292 bits (748), Expect = 4e-78
Identities = 148/150 (98%), Positives = 148/150 (98%)

- Query: 22 KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI 81
 - KAMEMVATSKMRKTODRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI
- Sbjct: 1 KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI 60
- Query: 82 STDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG 141

STDRGMCGGLNVNLFKT LNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG

- Sbjct: 61 STDRGMCGGLNVNLFKTILNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG 120
- Query: 142 DTPALEELIGVANTMFDAYRNGEIDAVYIA 171

D PALEELIGVANTMFDAYRNGEIDAVYIA

Sbjct: 121 DMPALEELIGVANTMFDAYRNGEIDAVYIA 150

tr <u>Q9RQ74</u> Gamma subunit of membrane-bound ATP synthase [ATPG] [Buchnera 289 AA aphidicola]

align

Score = 268 bits (684), Expect = 9e-71
Identities = 138/289 (47%), Positives = 199/289 (68%), Gaps = 3/289 (1%)

- Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
- M+ KE++ KI + +TQKITKAMEMV+ SKM+K + +M + RPY +TI+ +I++ + Sbjct: 1 MSEIKEVRNKIKCITNTQKITKAMEMVSISKMKKAEVKMNSGRPYLKTIKEIINNFISNN 60
- Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120

Y+H +L +R VKKIGI++ISTDRG+CG LNV LFK L+ I+N+ +NI++DL ++G

Sbjct: 61 TRYQHVYLEQRAVKKIGIIIISTDRGLCGNLNVTLFKKILDFIQNYNNRNITSDLSILGL 120

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Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
           KG+SFF+S
                                      + +
                                                  Y GEID +++AYNKF +T+
Sbjct: 121 KGLSFFKSLSNKIVYFNDYAKNNYTFSDCLNCNSIFMKLYSIGEIDRLFLAYNKFKSTLI 180
Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
           Q P + QL+PL + K
                           ++ WDY+YE + K+LL+ LL YLE QIYQA ++N S
Sbjct: 181 QIPSIIQLLPLSKKK---IHCHNNHWDYIYESDSKLLLNKLLNNYLEFOIYOASLENYTS 237
Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
           EQAARM+AMK ATDN+ +LI +L+++YNKARQ +IT EL EIV+GAAAI
Sbjct: 238 EQAARMIAMKQATDNSKDLIRELQIIYNKARQDNITQELTEIVSGAAAI 286
tr Q8D3J4 AtpG protein [ATPG] [Wigglesworthia glossinidia brevipalpis] 287 AA
                                                                        align
 Score = 265 \text{ bits } (676), Expect = 8e-70
 Identities = 135/286 (47%), Positives = 199/286 (69%), Gaps = 3/286 (1%)
          MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
Query: 1
              K+I+ KI ++ TQ IT AME ++ KM+K+O+ + +++PY E I +++ +
Sbjct: 1
          MYNIKDIRQKIIGIKKTQSITSAMEKISAIKMKKSQNLLNSTKPYYEKISLLLNKLLFQN 60
Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
           I YKHP+L +R++K IG +V+STDRG+ G LN+NLFK L +I
                                                         KE+ T+T L LIGS
Sbjct: 61 IKYKHPYLKKRQIKCIGYIVVSTDRGLAGSLNINLFKKLLYEINKSKEKKINTKLVLIGS 120
Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
           K ISFFR F
                      Ι
                           +SG+GDTP + ELI
                                                 Y + ID +YI NKF+NTM+
                                             М
Sbjct: 121 KAISFFRFFEDEIISTISGIGDTPKISELIKPVQIMLKEYDSNIIDKIYIISNKFINTMT 180
Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
             P ++++P+
                       K
                              + + + + +YLYEP+
                                              L +S+L RY+ES IYQ++V+N++S
Sbjct: 181 YVPDIKKVLPISIKKS---SIKFKNLNYLYEPDFSSLFESILPRYIESLIYQSIVENISS 237
Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGA 286
          EQ+ARMVAMK+A DN+ NLI +L L+YNKARQ++IT EL EI+AG+
Sbjct: 238 EQSARMVAMKSAMDNSKNLIEELSLIYNKARQSNITKELTEIIAGS 283
sp Q89B40
              ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Buchnera
                                                                           291
   ATPG BUCBP aphidicola
                                                                           AΑ
                                                                           align
               (subsp. Baizongia pistaciae)]
Score = 261 bits (667), Expect = 9e-69
Identities = 132/289 (45%), Positives = 202/289 (69%), Gaps = 1/289 (0%)
Query: 1
          MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
          M G +EI++K+ S+ +T+KITKAMEMV+ SK+RK + RM +SRPY
                                                          I VISHV
Sbjct: 1
          MIGIREIRSKMKSINNTKKITKAMEMVSISKLRKIKKRMCSSRPYFNIINQVISHVITGN 60
Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
          + + H + +R VK+IG++++STDRG+CG LN LFK L +
Sbjct: 61 LEHYHTYFNQRNVKRIGVIIVSTDRGLCGNLNTLLFKKVLEVLTEHINEHILNNLFVIGT 120
```

```
Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
           K ++FF+SF NI LS L + + +L+ + + Y +G+ID +++AYNKF +T+
Sbjct: 121 KALTFFKSFTNNIVFSLSNLKNDFKIIDLMEMIRISLEMYISGKIDKLFLAYNKFNSTII 180
Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
           O P + OL+P+ + K E ++TWDY+YE KVLL+ +L RY+E OIYO++++N+
Sbjct: 181 QTPTLVQLLPILKPKLGK-KEVKKTWDYIYESNSKVLLNVVLNRYIEFQIYQSILENLVC 239
Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
           EQA+RM+AMK ATDN+ +L+ L++ YNK RQ+SIT EL EI++GAAA+
Sbjct: 240 EQASRMLAMKQATDNSADLLKALQMNYNKVRQSSITQELTEIISGAAAV 288
tr <u>Q9RQ77</u> Gamma subunit of membrane-bound ATP synthase [ATPG] [Buchnera 290 AA
           aphidicola]
                                                                        align
 Score = 256 bits (654), Expect = 3e-67
 Identities = 127/289 (43%), Positives = 197/289 (67%), Gaps = 2/289 (0%)
Query: 1
          MAGAKEIKTKIASVOSTOKITKAMEMVATSKMRKTODRMAASRPYSETIRNVISHVSKAS 60
          M+ KEIK KI + +T+KITKAMEMV+ +KM+K++ +M + +PY + I+ +ISH+
Sbjct: 1
          MSEKKEIKNKINCISNTKKITKAMEMVSIAKMKKSEIKMKSRKPYLDIIKTIISHILYNH 60
Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNOIKNWKEONISTDLGLIGS 120
           I Y+H +L R+ KKIGI+VISTDRG+CG LN++LFK + I +K +N+ + L ++GS
Sbjct: 61 IKYRHLYLNNRKTKKIGIIVISTDRGLCGSLNISLFKKIIQLINIYKNKNVMSSLFILGS 120
Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
           KG+S+F+S ++I
                           + + + + + Y
                                                     +ID ++++YN+F NT+
Sbjct: 121 KGVSYFKSSTYDITYYEKIITKNYTFFDCLNFIHSSLEYYNTQKIDKLFLSYNQFKNTLV 180
Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
            PV+ QL+PL SK
                           + WDY+YE
                                             +LLD+LL Y+ESQIYQ++++N
Sbjct: 181 YIPVIMQLLPL--SKKIFKGNKNSHWDYIYESNSGILLDTLLNDYIESOIYOSILENCTC 238
Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
          EQA+RM++MK ATDN+ +LI LR++YNKARO +IT EL EI++GA A+
Sbjct: 239 EQASRMISMKQATDNSEDLIKKLRILYNKARQDNITQELTEIISGANAV 287
tr Q831A4 ATP synthase F1, gamma subunit [ATPG] [Enterococcus faecalis 302 AA
           (Streptococcus faecalis)]
                                                                       align
 Score = 218 bits (555), Expect = 8e-56
 Identities = 118/301 (39%), Positives = 180/301 (59%), Gaps = 15/301 (4%)
Query: 2
          AGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHV---- 56
              EIK +IAS + T +ITKAM+MV+ +K+ K++
                                                + + YS IR+V++H+
Sbjct: 3
          ASLNEIKQRIASTKKTSQITKAMQMVSAAKLTKSEGASKSFQEYSSKIRSVVTHLVAAQL 62
```

Query: 57 -----SKASIGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKE 108

S S G H L +R VKK G +VI++D+G+ GG N ++ K T++ I+

```
Sbjct: 63 SELRETEQSSLSEGNYHVMLAQRPVKKTGYIVITSDKGLVGGYNSSILKQTMSMIQEDHD 122
Query: 109 QNISTDLGLIGSKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAV 168
                L IG G FF++ G ++ +L GL D P EE+ + T
                                                             V+N
Sbjct: 123 SNKEYALIAIGGTGADFFKARGIDVSYELRGLTDQPTFEEVRKIVTTATTMYQNEVFDEL 182
Ouery: 169 YIAYNKFVNTMSQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLES 228
          Y+ YN VN+++ + V++++P+ + +Q +YL EP P+ +LD LL +Y ES
Sbjct: 183 YVCYNHHVNSLTSQFRVEKMLPITDLDPSEATSYEQ--EYLLEPSPEAILDQLLPQYAES 240
Query: 229 QIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAA 288
                     +E AA M AMK ATDNA N+I+DL + YN+ARQ +IT E+ EIVAGAAA
Sbjct: 241 LIYGAIIDAKTAEHAAGMTAMKTATDNAQNIISDLTISYNRARQGAITQEITEIVAGAAA 300
Query: 289 I 289
Sbjct: 301 L 301
sp P20602
              ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Bacillus
                                                                          285
   ATPG BACME megaterium]
                                                                          AΑ
                                                                          align
Score = 216 bits (549), Expect = 4e-55
Identities = 117/289 (40%), Positives = 175/289 (60%), Gaps = 5/289 (1%)
          MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
Query: 1
          MA ++I+T+I S + T +ITKAMEMV+ +K+ + + PY E I+ V+S V+ S
Sbjct: 1
          MASLRDIQTRITSTKKTSQITKAMEMVSAAKLNRAEQNAKSFVPYMEKIQEVVSSVALGS 60
Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
           G HP L R VKK G +VI++DRG+ G N N+ +
                                                    \mathbf{I} +
Sbjct: 61 RGASHPMLTARSVKKTGYIVITSDRGLAGAYNSNILRKVSQAIEERHQSPDEYGVIAIGR 120
Ouery: 121 KGISFFRSFGFNIKGOLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
           G FF
                   G + +++GL D PA ++ G+A+
                                                + +G D +Y+ YN F+NT+S
Sbjct: 121 VGRDFFVKRGIPVLLEITGLADQPAFADIQGIASQTVQMFADGTFDELYLYYNHFINTIS 180
Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
          0+
               ++L+PL +
                            L + Y +EP + +L+ LL +Y ES IY ++D AS
Sbjct: 181 QEVTEKKLLPLTD-----LQPSGKLVGYEFEPSQEEILEVLLPQYAESLIYGGLLDGKAS 235
Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
          E AARM AMK+ATDNA +LIN+L L YN+ARQA+IT E+ EIV GAAA+
Sbjct: 236 EHAARMTAMKSATDNAKDLINNLTLSYNRARQAAITQEITEIVGGAAAL 284
trnew AAQ10089 ATP synthase subunit gamma [ATPG] [Bacillus sp. TA2.A1] 286 AA
                                                                       align
Score = 211 bits (536), Expect = 1e-53
Identities = 114/289 (39%), Positives = 182/289 (62%), Gaps = 4/289 (1%)
Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
```

```
M G +EIK +I SV++T++ITKAM+MVA +K+R+ Q+
                                                 +RPY++ I+ VIS ++ +
          MQGMREIKRRIRSVKNTRQITKAMKMVAAAKLRRAQETAENARPYADKIKEVISSIAAGT 60
Sbjct: 1
Ouery: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNOIKNWKEONISTDLGLIGS 120
            + HP L R VKK G +VI++DRG+ G N N+ +
                                                 I +
Sbjct: 61 KDFSHPMLEARPVKKTGYMVITSDRGLAGPYNANILRLVSKTIEERHQSKDEYVIFAVGR 120
Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
          KG FF+ G+ + +++G+ DTP+L E+ +A +
                                                + +
                                                      D + I YN+FV+ +
Sbjct: 121 KGRDFFKKRGYPVVEEVTGISDTPSLTEIQDIAQSAIGMFADETFDKLTIFYNEFVSPIV 180
Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
          Q+PV+QL+PL+++L+ Y YEP+ + +L+ LL +Y E+ IY A++D AS
Sbjct: 181 QRPVEKQLLPL--TSEEVLDGPVSA--YEYEPDSESVLEVLLPKYAETLIYSALLDAKAS 236
Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
          E ARM AM ATDNA ++ L L +N+ARQA+IT E+ EIVAGA A+
Sbjct: 237 EFGARMTAMGNATDNATEMLETLTLQFNRARQAAITQEIAEIVAGANAL 285
```

tr Q8E5U9 H+-transporting ATP synthase gamma chain [ATPG] [Streptococcus 293 AA agalactiae (serotype III)]

Score = 210 bits (535), Expect = 2e-53

align

```
Identities = 113/292 (38%), Positives = 181/292 (61%), Gaps = 3/292 (1%)
          MAGA-KEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKA 59
Query: 1
          MAG+ EIK KI S + T KIT AM+MV+++K+ K++
                                                    + Y+ IR + +++ K+
Sbjct: 1
          MAGSLSEIKDKILSTEKTSKITSAMQMVSSAKLVKSEQAARDFQVYASKIRQITTNLLKS 60
Query: 60 SI--GYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGL 117
           + G +P L R VKK G +VI++D+G+ GG N + K ++ I ++ +N
Sbjct: 61 DLVSGSDNPMLASRPVKKTGYIVITSDKGLVGGYNSKILKAMMDTITDYHTENDDYAIIS 120
Query: 118 IGSKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVN 177
          IGS G FF++ G N+ +L GL D P+ +++ + + Y+N
                                                         D + Y + YN VN
Sbjct: 121 IGSVGSDFFKARGMNVSFELRGLEDQPSFDQVGKIIAQAVEMYKNELFDELYVCYNHHVN 180
Query: 178 TMSQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDN 237
          +++ + +QQ++P+ E
                           D + E + EP + V + LL + Y ES IY A + + D
Sbjct: 181 SLTSQVRMQQMLPIKELDADEASEDRVITGFELEPNREVILEQLLPQYTESLIYGAIIDA 240
Query: 238 VASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
            +E AA M AM+ ATDNA N+INDL + YN+ARQA+IT E+ EIVAGA A+
Sbjct: 241 KTAEHAAGMTAMQTATDNAKNVINDLTIQYNRARQAAITQEITEIVAGANAL 292
```

```
sp <u>Q9K6H4</u> ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Bacillus 285 ATPG_BACHD halodurans] AA align
```

Score = 209 bits (532), Expect = 4e-53Identities = 113/289 (39%), Positives = 176/289 (60%), Gaps = 5/289 (1%)

tr	Q81	<u>4W1</u>	ATP synthase gamma chain (EC 3.6.3.14) [BC5307] [Bacillus cereus	286 AA
Sbjo	ct:	241	+E AA M AM+ ATDNA N+INDL + YN+ARQA+IT E+ EIVAGA A+ KTAEHAAGMTAMQTATDNAKNVINDLTIQYNRARQAAITQEITEIVAGANAL 292	
Quei	ry:	238	VASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289	
Sbjo	ct:	181	+++ + +QQ++P+ E + +E + + EP +V+L+ LL +Y ES IY A++D SLTSQVRMQQMLPIKELDAEEASEDRVITGFELEPNREVILEQLLPQYTESLIYGAIIDA	240
Quei	ry:	178	TMSQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDN	237
Sbjo	ct:	121	$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	180
Quei	ry:	118	IGSKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVN	177
Sbjo	ct:	61	+ G +P L R VKK G +VI++D+G+ GG N + K ++ I ++ +N + DLVSGSDNPMLSSRPVKKTGYIVITSDKGLVGGYNSKILKAMMDTITDYHTENDDYAIIS	120
Quei	ry:	60	SIGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGL	117
Sbjo	ct:	1	MAG+ EIK KI S + T KIT AM+MV+++K+ K++ + Y+ IR + +++ K+ MAGSLSEIKDKILSTEKTSKITSAMQMVSSAKLVKSEQAARDFQVYASKIRQITTNLLKS	60
Quei	ry:	1	MAGA-KEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKA	59
			208 bits (529), Expect = 9e-53 s = 112/292 (38%), Positives = 181/292 (61%), Gaps = 3/292 (1%	;)
			agalactiae (serotype V)]	AA align
tr	Q8E	073	ATP synthase F1, gamma subunit [ATPG] [Streptococcus	293
Sbj	ct:	236	EFAARMTAMSAATDNATNLIDELTLSYNRARQAAITQEITEIVGGAAAL 284	
Que	ry:	241	EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289 E AARM AM AATDNA NLI++L L YN+ARQA+IT E+ EIV GAAA+	
Sbj	ct:	181	QDVTEKKVLPLTDLSDTKVSTTYEYEPNEQVILEALLPQYAESLVYGALLDAKAS	235
Que	ry:	181	QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS Q ++++PL + L++ + Y YEP +V+L++LL +Y ES +Y A++D AS	240
Sbjo	ct:	121	TGRDLLKKRQLPIISEMTGLSDQPTFNDIKDIAKQTVDMFADEVFDELYIWYNHFVSPIK	180
Que	ry:	121	KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS G + I +++GL D P ++ +A D ++ D +YI YN FV+ +	180
Sbjo	ct:	61	TDVSHPMLEERPVKKTGYIVITSDRGLAGAYNSNLIRGLLYTINKRHKSKDEYGIFAIGR	120
Que	ry:	61	IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS HP L ER VKK G +VI++DRG+ G N NL + L I + + IG	120
Sbjo	ct:	1	MASLRDIKQRINSTKKTKQITKAMEMVSAAKLNRSQEKAQSFLPYTDKIREVVASIAASD	60
Que	ry:	1	MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS MA ++IK +I S + T++ITKAMEMV+ +K+ ++Q++ + PY++ IR V++ ++ +	60

(strain ATCC 14579 / DSM 31)]

Identities = 113/290 (38%), Positives = 177/290 (60%), Gaps = 6/290 (2%)

Score = 207 bits (528), Expect = 1e-52

align

Query:	1	MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS MA ++IK KI S + T +ITKAMEMV+ SK+ + + PY E I+ V++ +++ S	60
Sbjct:	1	MASLRDIKAKINSTKKTSQITKAMEMVSASKLNRAEQNAKSFVPYMEKIQEVVASIAQGS	60
Query:	61	IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNIST-DLGLIG G HP L R VK+ G +VI++DRG+ GG N N+ +T N I+ + + +++G	119
Sbjct:	61	KGINHPMLNARPVKRTGYIVITSDRGLAGGYNSNVLRTVSNVIRERHNMDSNQYSIIVLG	120
Query:	120	SKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTM G + + GFNI ++ GL D P+ ++ +A+ ++G D +YI YN +V+ +	179
Sbjct:	121	RLGRDYLKRRGFNIIDEVVGLSDHPSFTDIKDLASRAIAMFADGAYDELYIYYNHYVSKI	180
Query:	180	SQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVA SQ+ +++PL + D + T Y +EP + +L LL +Y ES +Y A++D A	239
Sbjct:	181	SQEVTENKILPLTDVASDKPTTAYEFEPSEEEILKVLLPQYAESLVYGALLDGKA	235
Query:	240	SEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289 SE AARM AMK+ATDNA +I+ L L +N+ARQA+IT E+ EIV GAAA+	
Sbjct:	236	SEHAARMTAMKSATDNAMEVIDSLTLSFNRARQAAITQEITEIVGGAAAL 285	
tr <u>Q81</u>	JZ4	ATP synthase F1, gamma subunit [ATPG] [Bacillus anthracis (strain Ames)]	286 AA align
		207 bits (528), Expect = 1e-52 s = 113/290 (38%), Positives = 177/290 (60%), Gaps = 6/290 (2%)
Query:	1	MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS (MA ++IK KI S + T +ITKAMEMV+ SK+ + + PY E I+ V++ +++ S	60
Sbjct:	1	MASLRDIKAKINSTKKTSQITKAMEMVSASKLNRAEQNAKSFVPYMEKIQEVVASIAQGS	60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNIST-DLGLIG 119
G HP L R VK+ G +VI++DRG+ GG N N+ +T N I+ + + ++G

Sbjct: 61 KGINHPMLNARPVKRTGYIVITSDRGLAGGYNSNVLRTVSNVIRERHNMDSNQYSIIVLG 120

Query: 120 SKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTM 179
G + + GFNI ++ GL D P+ ++ +A+ ++G D +YI YN +V+ +

Sbjct: 121 RLGRDYLKRRGFNIIDEVVGLSDHPSFTDIKDLASRAIAMFADGAYDELYIYYNHYVSKI 180

Query: 180 SQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVA 239 SQ+ +++PL + D + T Y +EP + +L LL +Y ES +Y A++D A

Sbjct: 181 SQEVTENKILPLTDVASD-----KPTTAYEFEPSEEEILKVLLPQYAESLVYGALLDGKA 235

Query: 240 SEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289 SE AARM AMK+ATDNA +I+ L L +N+ARQA+IT E+ EIV GAAA+

Sbjct: 236 SEHAARMTAMKSATDNAMEVIDSLTLSFNRARQAAITQEITEIVGGAAAL 285

trnew AAS44331 ATP synthase F1, gamma subunit (EC 3.6.3.14) [ATPG] 286
[Bacillus AA cereus ATCC 10987] align

Score = 207 bits (528), Expect = 1e-52

Identities = 113/290 (38%), Positives = 177/290 (60%), Gaps = 6/290 (2%) MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60 Query: 1 MA ++IK KI S + T +ITKAMEMV+ SK+ + + + PY E I+ V++ +++ S MASLRDIKAKINSTKKTSQITKAMEMVSASKLNRAEQNAKSFVPYMEKIQEVVASIAQGS 60 Sbjct: 1 Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEONIST-DLGLIG 119 G HP L R VK+ G +VI++DRG+ GG N N+ +T N I+ + + ++G Sbjct: 61 KGINHPMLNARPVKRTGYIVITSDRGLAGGYNSNVLRTVSNVIRERHNMDSNQYSIIVLG 120 Query: 120 SKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTM 179 G + + GFNI ++ GL D P+ ++ +A+ + +G D +YI YN +V+ + Sbjct: 121 RLGRDYLKRRGFNIIDEVVGLSDHPSFTDIKDLASRAIAMFADGAYDELYIYYNHYVSKI 180 Query: 180 SQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESOIYOAVVDNVA 239 +++PL + D + T Y +EP + +L LL +Y ES +Y A++D A SO+ Sbjct: 181 SQEVTENKILPLTDVASD-----KPTTAYEFEPSEEEILKVLLPQYAESLVYGALLDGKA 235 Query: 240 SEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289 SE AARM AMK+ATDNA +I+ L L +N+ARQA+IT E+ EIV GAAA+ Sbjct: 236 SEHAARMTAMKSATDNAMEVIDSLTLSFNRARQAAITQEITEIVGGAAAL 285 tr Q9RAU1 H+-ATPase cytoplasmic F1-part gamma-subunit (H+-ATPase gamma 289 AA subunit) [ATPG] [Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris), Lactococcus lactis (subsp. align lactis) (Streptococcus lactis)] Score = 206 bits (525), Expect = 3e-52 Identities = 110/289 (38%), Positives = 176/289 (60%), Gaps = 3/289 (1%) Query: 2 AGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISH-VSKAS 60 EIKTKIAS + T +IT AM+MV+ +K++K + A + Y + E + R + + VS +Sbjct: 3 ASLNEIKTKIASTKKTSQITGAMQMVSAAKLQKAESHAKAFQTYAEKVRKITTDLVSSDN 62 Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNOIKNWKEONISTDLGLIGS 120 K+P +++REVKK G LVI++DRG+ G N N+ K+ ++ I+ Sbjct: 63 EPAKNPMMIKREVKKTGYLVITSDRGLVGSYNSNILKSVISNIRKRHTNESEYTILALGG 122 Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180 G FF++ + L GL D P EE+ + + Y+ E D +Y+ YN VN++ Sbjct: 123 TGADFFKARNVKVSYVLRGLSDQPTFEEVRAIVTEAVEEYQAEEFDELYVCYNHHVNSLV 182 Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240 + +++++P+ S D+ +E+ + EP+ + +L+ LL +Y ES IY ++VD Sbjct: 183 SEARMEKMLPI--SFDEKGDEKASLVTFELEPDRETILNQLLPQYAESMIYGSIVDAKTA 240 Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289 E AA M AM+ ATDNA ++INDL + YN+ARQASIT E+ EIVAGA+A+ Sbjct: 241 EHAAGMTAMRTATDNAHSVINDLTIQYNRARQASITQEITEIVAGASAL 289 tr Q8EM82 H(+)-transporting ATP synthase gamma chain (EC 3.6.1.34) 286 AA [Oceanobacillus iheyensis] align

```
ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Lactococcus
sp Q9CER9
   ATPG LACLA lactis
                                                                           AΑ
                                                                           align
               (subsp. lactis) (Streptococcus lactis)]
 Score = 205 bits (521), Expect = 7e-52
 Identities = 110/289 (38%), Positives = 172/289 (59%), Gaps = 3/289 (1%)
Query: 2
          AGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISH-VSKAS 60
               EIKTKIAS + T +IT AM+MV+ +K++K +
                                                 A + Y + E + R + + VS
Sbjct: 3
          ASLNEIKTKIASTKKTSQITGAMQMVSAAKLQKAESHAKAFQIYAEKVRKITTDLVSSDK 62
Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEONISTDLGLIGS 120
              K+P +++REVKK G LVI++DRG+ GG N N+ K+ +N I+
          EPAKNPMMIKREVKKTGYLVITSDRGLVGGYNSNILKSVMNTIRKRHANESEYTILALGG 122
Sbjct: 63
Query: 121 KGISFFRSFGFNIKGOLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
            G FF++
                          L GL D P EE+ +
                                                 Y+ E D +Y+ YN VN++
Sbjct: 123 TGADFFKARNVKVSYVLRGLSDQPTFEEVRAIVTEAVTEYQAEEFDELYVCYNHHVNSLV 182
Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
               ++++P+
                                 +T++
                                        EP+ + +L+ LL +Y ES IY ++VD
Sbjct: 183 SDARMEKMLPISFEESGQQKPSLETFEL--EPDRETILNQLLPQYAESMIYGSIVDAKTA 240
Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
           E AA M AM+ ATDNA ++INDL + YN+ARQASIT E+ EIVAGA+A+
```

sp P22482 ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Bacillus 289 AA ATPG_BACPF pseudofirmus]

Sbjct: 241 EHAAGMTAMRTATDNAHSVINDLTIQYNRARQASITQEITEIVAGASAL 289

Score = 205 bits (521), Expect = 7e-52

align

```
Identities = 112/291 (38%), Positives = 175/291 (59%), Gaps = 5/291 (1%)
Query: 1
          MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
          MA ++I++I S + T++ITKAM+MV++K++Q
                                               + PY++ IR V++ ++ +
Sbjct: 1
          MASLRDIQGRITSTKKTKQITKAMQMVSAAKLNRAQHNAQSFTPYTDKIREVVAAIASSG 60
Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLI-- 118
              HP L ER VKK G +V+++D+G+ GG N +L ++ LN IK + N
Sbjct: 61 TEISHPMLEERPVKKTGYIVVTSDKGLAGGYNSSLIRSLLNTIK--ERHNSPDEYGIIIM 118
Query: 119 GSKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNT 178
                F+ G I ++ GL D P ++ +A T + ++G D +Y+ YN FV+
Sbjct: 119 GRIGRDLFKKRGLPIIQEVIGLPDQPEFNDIKNIARTSVEMFADGIFDELYVWYNHFVSP 178
Query: 179 MSQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNV 238
                  +L+PL + D
                                   + Y YEP + +L+ LL +Y ES IY +++D
Sbjct: 179 ITQDVTEMKLLPLTDIGSDE-KATSASASYEYEPNEQAILEKLLPQYAESLIYGSLLDAK 237
Query: 239 ASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
          ASE ARM AM AATDNA LI +L L +N+ARQA+IT E+ EIV GAAA+
Sbjct: 238 ASEFGARMTAMSAATDNASALIEELTLKFNRARQAAITOEITEIVGGAAAL 288
```

tr Q8CNJ6 ATP synthase gamma chain [SE1701] [Staphylococcus epidermidis] 288 AA

align

Score = 205 bits (521), Expect = 7e-52
Identities = 105/289 (36%), Positives = 178/289 (61%), Gaps = 2/289 (0%)

- Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
 MA KEI ++I S ++ITKAM MV++SK+R+ + + RPY E +++ I+ V+ ++
- Sbjct: 1 MASLKEIDSRIKSTSKMKQITKAMNMVSSSKLRRAEKNTKSFRPYMEKMQDAITAVAGSN 60
- Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120 HP L R++K+ G LVI++D+G+ G + N+ K+ +N I + + L ++G
- Sbjct: 61 STSNHPMLKSRDIKRSGYLVITSDKGLAGAYSTNVLKSLVNDINSKHNDSSEYSLIVLGQ 120
- Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180 +G+ FF+ G+ I+ L + D P+ + + +A D + ID + I Y+ +V+ +
- Sbjct: 121 QGVDFFKHRGYEIESSLVEVPDQPSFKSIQSIAKHAIDLFSEENIDELTIYYSHYVSVLE 180
- Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240 KP +Q++PL S++D Q Y +EP+ + +L +L +Y+ES IY ++D AS
- Sbjct: 181 NKPATKQVLPL--SQEDSGQGHGQMSSYEFEPDKESILSVILPQYVESLIYGTILDAKAS 238
- Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
- E A+RM AM+ A+DNA LI+DL L YN+ARQA+IT ++ EIV G++A+ Sbjct: 239 EHASRMTAMRNASDNATELIDDLSLEYNRARQAAITQQITEIVGGSSAL 287

tr 005432 ATP synthase subunit gamma [ATPG] [Moorella thermoacetica 282 AA (Clostridium thermoaceticum)]

align

Score = 204 bits (520), Expect = 1e-51 Identities = 114/289 (39%), Positives = 172/289 (59%), Gaps = 8/289 (2%)

- Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60 MA +++K +I SVQSTQ IT+AM+MVA +K+RK Q ++ A RPY+ + V+ + A
- Sbjct: 1 MAHMRDLKRRIRSVQSTQHITRAMKMVAAAKLRKAQAQVTAGRPYAAKLEEVVGRLMAAV 60
- Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
 PREVKK G ++I+ DRG+ GG N NL + T +++ E+ L +G
- Sbjct: 61 DPETQPLAATREVKKAGYVLITADRGLAGGYNANLIRLTEERLR---EEGRPAALVAVGR 117
- Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
- KG FFR I + +GD P L + +A + Y G +D V + +F + + Sbjct: 118 KGRDFFRRRPVEIVKSFTDIGDNPELIQARELARQLVTMYLEGTLDEVNLINTRFYSPIR 177
- Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
- Q P+V++L+P+ + E++ T DY+YEP P+ +L LL RY E ++Y+A+++ AS Sbjct: 178 QVPMVERLLPIATPR----EKKDTGDYIYEPSPEGVLRVLLPRYCEIKVYRALLEAKAS 232
- Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
 - E ARM AM AT NA +I+ L +N+ARQA+ITNE+ EIVAGA A+
- Sbjct: 233 EHGARMTAMDNATKNAAEMIDKFTLSFNRARQAAITNEIVEIVAGADAL 281

ATP synthase gamma chain precursor (EC 3.6.3.14) [ATPG] sp P09222 286 ATPG BACP3 [Bacillus AΑ PS3 (Thermophilic bacterium PS-3)] align Score = 202 bits (513), Expect = 6e-51 Identities = 118/289 (40%), Positives = 173/289 (59%), Gaps = 7/289 (2%) Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60 +A ++IKT+I + + T +ITKAMEMV TSK+ + + R RPY E I+ V+++V+ A+ Sbjct: 4 LASLRDIKTRINATKKTSQITKAMEMVLTSKLNRAEKREIV-RPYMEKIQEVVANVALAA 62 Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120 HP LV R VKK G LVI++DRG+ G N N+ + Sbjct: 63 RA-SHPMLVSRPVKKTGYLVITSDRGLAGAYNSNVLRLVYQTIQKRHASPDEYAIIVIGR 121 Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180 + ++ L D P+ ++ +A + +G D +Y+ YN +V+ + G+SFFR Sbjct: 122 VGLSFFRKRNMPVILDITRLPDQPSFADIKEIARKTVGLFADGTFDELYMYYNHYVSAIQ 181 Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240 ++L+PL + L E +Q Y +EP + +LD LL +Y ES IY A++D AS Sbjct: 182 QEVTERKLLPLTD-----LAENKQRTVYEFEPSQEEILDVLLPQYAESLIYGALLDAKAS 236 Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKAROASITNELNEIVAGAAAI 289 E AARM AMK ATDNA LI L L YN+ARQA+IT E+ EIVAGA A+ Sbjct: 237 EHAARMTAMKNATDNANELIRTLTLSYNRARQAAITQEITEIVAGANAL 285 tr Q9A018 Putative proton-translocating ATPase, gamma subunit (EC 291 3.6.1.34) [ATPG] [Streptococcus pyogenes, Streptococcus pyogenes align (serotype M18)] Score = 201 bits (512), Expect = 8e-51 Identities = 115/292 (39%), Positives = 177/292 (60%), Gaps = 5/292 (1%) Query: 1 MAGA-KEIKTKIASVQSTQKITKAMEMVATSKMRKTODRMAASRPYSETIRNVISHVSKA 59 $MAG+EIK\ KI\ S+T\ KIT\ AM\ MV+++K+\ K++$ + Y+ IR + + K+ Sbjct: 1 MAGSLSEIKAKIISTEKTSKITSAMRMVSSAKLVKSEQAARDFQIYASKIRQITTDLLKS 60 --SIGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGL 117 Query: 60 +IG +P LV R VKK G +VI++D+G+ GG N + K+ ++ I + Sbjct: 61 ELTIGSDNPMLVSRPVKKTGYIVITSDKGLVGGYNSKILKSVMDMITEYHADG-DYEIIS 119 Query: 118 IGSKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVN 177 IGS G FF++ G N+ +L GL D P+ E++ + + D + N D +Y+ YN VN Sbjct: 120 IGSVGSDFFKARGMNVAFELRGLADQPSFEQVRQIISQSVDMFVNEIFDELYVCYNHHVN 179 Query: 178 TMSQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDN 237 +++ + VQQ++P+ + D E T + EP +LD LL ++ ES IY A++D Sbjct: 180 SLTSQVRVQQMLPISDLVADEAAEEGVT-GFELEPNRHDILDQLLPQFTESLIYGAIIDA 238 Query: 238 VASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289 +E AA M AM+ ATDNA N+INDL + YN+ARQA+IT E+ EIVAGA A+ Sbjct: 239 KTAEHAAGMTAMQTATDNAKNVINDLTIQYNRARQAAITQEITEIVAGANAL 290

```
TF1-gamma subunit [thermophilic bacterium PS3] 282 AA
tr
     Q52412
                                                                align
 Score = 201 bits (511), Expect = 1e-50
 Identities = 118/288 (40%), Positives = 172/288 (58%), Gaps = 7/288 (2%)
          AGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASI 61
Query: 2
          A ++IKT+I + + T +ITKAMEMV TSK+ + + R
                                                  RPY E I+ V+++V+ A+
Sbjct: 1
         ASLRDIKTRINATKKTSQITKAMEMVLTSKLNRAEKREIV-RPYMEKIQEVVANVALAAR 59
Query: 62 GYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSK 121
             HP LV R VKK G LVI++DRG+ G N N+ +
                                                   Ι+
                                                               + + IG
Sbjct: 60 A-SHPMLVSRPVKKTGYLVITSDRGLAGAYNSNVLRLVYQTIQKRHASPDEYAIIVIGRV 118
Query: 122 GISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMSQ 181
          G+SFFR + ++ L D P+ ++ +A
                                               + +G D +Y + YN +V + + Q
Sbjct: 119 GLSFFRKRNMPVILDITRLPDQPSFADIKEIARKTVGLFADGTFDELYMYYNHYVSAIQQ 178
Query: 182 KPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVASE 241
              ++L+PL+ L E +Q Y +EP + +LD LL +Y ES IY A++D ASE
Sbjct: 179 EVTERKLLPLTD-----LAENKQRTVYEFEPSQEEILDVLLPQYAESLIYGALLDAKASE 233
Query: 242 QAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
           AARM AMK ATDNA LI L L YN+ARQA+IT E+ EIVAGA A+
Sbjct: 234 HAARMTAMKNATDNANELIRTLTLSYNRARQAAITQEITEIVAGANAL 281
sp P37810
              ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Bacillus
                                                                         290
   ATPG BACSU subtilis]
                                                                         AΑ
                                                                         align
 Score = 201 bits (510), Expect = 1e-50
 Identities = 110/289 (38%), Positives = 175/289 (60%), Gaps = 3/289 (1%)
Query: 1
          MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
          +A ++IK++IS + T +ITKAM+MV+ +K+ + ++ + + PY + I+ V+S+V + S
          LASLRDIKSRITSTKKTSQITKAMQMVSAAKLNRAENNAKSFVPYMDKIQEVVSNVGRVS 63
Sbjct: 4
Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEONISTDLGLIGS 120
             KHP L+ REVKK LVI++DRG+ G N ++ ++
                                                   ++
                                                       4-
                                                               + TG
Sbjct: 64 GNVKHPMLLSREVKKTAYLVITSDRGLAGAFNSSVLRSAYQAMQERHQSKDEYAVIAIGR 123
Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
                                 E+ +A
           G FF+
                     I +L+GLGD
                                                + +G D +++ YN FV+ ++
Sbjct: 124 VGRDFFKKREIPIISELTGLGDEVTFTEIKDLARQTIQMFIDGAFDELHLVYNHFVSAIT 183
Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
              ++L+PL
                      D ++T Y +EP + +L+ LL +Y ES I+ A++D+ AS
Sbjct: 184 QEVTEKKLLPL---SDLGSGGGKRTASYEFEPSEEEVLEVLLPQYAESLIFGALLDSKAS 240
Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
          E AARM AMK ATDNA LI+ L L YN+ARQA+IT E+ EIV GAAA+
Sbjct: 241 EHAARMTAMKNATDNAKELIDSLSLSYNRARQAAITQEITEIVGGAAAL 289
```

tr <u>Q99</u>	<u> 98F4</u>	Mu50 / ATCC 700699), Staphylococcus aureus (strain N315), Staphylococcus aureus (strain NW2)]	AA align
		201 bits (510), Expect = 1e-50 s = 106/289 (36%), Positives = 174/289 (59%), Gaps = 2/289 (0%	k)
Query:	1	MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS MA KEI T+I S + ++ITKAM MV++SK+R+ + PY + +++ I+ V+ AS	60
Sbjct:	1	MASLKEIDTRIKSTKKMKQITKAMNMVSSSKLRRAEKNTKQFTPYMDKMQDAITAVAGAS	60
Query:		IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS HP L R++ + G LVI++D+G+ G + N+ K + I+ + + + ++G	
Sbjct:	61	SNTNHPMLRPRKITRSGYLVITSDKGLAGAYSANVLKKLITDIEAKHQDSSEYSIVVLGQ	120
Query:	121	KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS +G+ F ++ G++I+ + D P+ + + +AN D Y EID + I Y+ +V+ +	180
Sbjct:	121	QGVDFLKNRGYDIEYSQVDVPDQPSFKSVQALANHAIDLYSEEEIDELNIYYSHYVSVLE	180
Query:	181	QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS KP +Q++PL S++D Y +EP+ + +L +L +Y+ES IY ++D AS	240
Sbjct:	181	NKPTSRQVLPLSQEDSSKGHGHLSSYEFEPDKESILSVILPQYVESLIYGTILDAKAS	238
Query:	241	EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289 E A RM AMK ATDNA LI+DL L YN+ARQA IT ++ EIV G+AA+	
Sbjct:	239	EHATRMTAMKNATDNATELIDDLSLEYNRARQAEITQQITEIVGGSAAL 287	
tr <u>050</u>	158	Proton-translocating ATPase, gamma subunit [ATPG] [Streptococcus bovis]	291 AA align
		201 bits (510), Expect = 1e-50 s = 115/292 (39%), Positives = 178/292 (60%), Gaps = 5/292 (1%	s)
Query:	1	MAGA-KEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKA MAG+ EIK KI S Q T IT AM+MV+ +K+ K++ + Y+ IR + + + K+	59
Sbjct:	1	MAGSLSEIKGKIISTQKTSHITGAMQMVSAAKLTKSEQAAKDFQVYASKIRQITTDLLKS	60
Query:		SIGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGL + G K+P L R VKK G +VI++D+G+ GG N + K ++ I+ + O+ + +	117
Sbjct:		ELVNGSKNPMLAARPVKKTGYIVITSDKGLVGGYNSKILKAMMDLIEEY-HQDGNYAIIA	119
Query:	118	IGSKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVN IG G FF++ G N+ +L GL D P+ E++ + + Y+N D +Y+ YN VN	177
Sbjct:	120	IGGIGADFFKARGMNVVFELRGLEDQPSFEQVGNIIAKSVEMYKNELFDELYVCYNHHVN	179
Query:	178	TMSQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDN	237
Sbjct:	180	+++ + VQQ++P+ E D E + + EP +++L+ LL +Y ES IY A+VD SLTSQVRVQQMLPIAELDADEAAEEGVS-GFELEPNREMILEQLLPQYTESLIYGAIVDA	238
_	238	VASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289	

+E AA M AM+ ATDNA N+INDL + YN+ARQA+IT E+ EIVAGA A+ Sbjct: 239 KTAEHAAGMTAMQTATDNAKNVINDLTIQYNRARQAAITQEITEIVAGANAL 290

tr Q8K827 Putative proton-translocating ATPase gamma subunit 291 [SPYM3 0498] AA [Streptococcus pyogenes (serotype M3)] align Score = 200 bits (509), Expect = 2e-50 Identities = 114/292 (39%), Positives = 177/292 (60%), Gaps = 5/292 (1%) MAGA-KEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKA 59 Query: 1 MAG+ EIK KI S + T KIT AM MV+++K+ +++ + Y+ IR + + + K+ Sbjct: 1 ${\tt MAGSLSEIKAKIISTEKTSKITSAMRMVSSAKLVRSEQAARDFQIYASKIRQITTDLLKS} {\tt 60}$ Query: 60 --SIGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGL 117 +IG +P LV R VKK G +VI++D+G+ GG N + K+ ++ I + Sbjct: 61 ELTIGSDNPMLVSRPVKKTGYIVITSDKGLVGGYNSKILKSVMDMITEYHADG-DYEIIS 119 Query: 118 IGSKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVN 177 IGS G FF++ G N+ +L GL D P+ E++ + + D + N D +Y+ YN VN Sbjct: 120 IGSVGSDFFKARGMNVAFELRGLADQPSFEQVRQIISQSVDMFVNEIFDELYVCYNHHVN 179 Query: 178 TMSQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESOIYOAVVDN 237 +++ + VQQ++P+ + D E T + EP +LD LL ++ ES IY A++D Sbjct: 180 SLTSQVRVQQMLPISDLVADEAAEEGVT-GFELEPNRHDILDQLLPQFTESLIYGAIIDA 238 Query: 238 VASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289 +E AA M AM+ ATDNA N+INDL + YN+ARQA+IT E+ EIVAGA A+ Sbjct: 239 KTAEHAAGMTAMQTATDNAKNVINDLTIQYNRARQAAITQEITEIVAGANAL 290

tr Q84XB4 Chloroplast ATPase gamma subunit precursor [ATPC] [Phaeodactylum tricornutum]

Score = 200 bits (508), Expect = 2e-50

369 AA align

Identities = 114/312 (36%), Positives = 187/312 (59%), Gaps = 27/312 (8%) AKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGY 63 Query: 4 A I+ +I SV++T+KIT AM++VA +K+R+ QD + A+RP+SET+++VSbjct: 58 ANAIRDRITSVKNTRKITMAMKLVAAAKVRRAQDAVLATRPFSETLQSVFGGLIQRLGGE 117 Query: 64 KH--PFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSK 121 P L EREVKK+ +LVI+ DRG+CGG N + K + K K+ + DL L+G K Sbjct: 118 SVDLPLLTEREVKKVTLLVITGDRGLCGGYNSFMIKKAEARFKELKKNGVEADLILVGKK 177 Query: 122 GISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMSQ 181 G+ I+ + G P ++ +A + +GE DAV + Y KFV+ ++ Sbjct: 178 GIAYFERRGYPIRKKYE-TGQNPTAKQALAIAEEVSSTFLSGESDAVELLYTKFVSLIAS 236 Query: 182 KPVVQQLVPLPES----KDDHLNE--------RQQTWDYLYEPEPKVL 217 P ++ LVP S K D + + D ++E +P + Sbjct: 237 SPSIRTLVPFSASDITAKGDEVFQLTSESGQFGVERTELDVAAPQEFPNDMIFEQDP1QI 296

Query: 218 LDSLLVRYLESQIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITN 277 ++++L YL QI + + ++VASE AARM +M++A+DNAG+L L L YN+AROA++T Sbjct: 297 VNAILPLYLNGQILRTLQESVASELAARMQSMQSASDNAGSLAKOLNLEYNRAROAAVTO 356 Query: 278 ELNEIVAGAAAI 289 EL EI++GA+A+ Sbjct: 357 ELLEIISGASAL 368 sp P12408 ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Anabaena 315 ATPG ANASP sp. (strain AΑ PCC 7120)] align Score = 198 bits (503), Expect = 9e-50 Identities = 114/315 (36%), Positives = 185/315 (58%), Gaps = 27/315 (8%) Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60 K I+ +I SV++T+KIT+AM +VA +++R+ Q+++ A+RP+++ + V+ Sbjct: 1 MPNLKSIRDRIQSVKNTKKITEAMRLVAAARVRRAQEQVIATRPFADRLAQVLYGL-QTR 59 IGYKH---PFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGL 117 Query: 61 P L +REVK +G+LVIS DRG+CGG N N+ + N+ K K + + Sbjct: 60 LRFEDVDLPLLKKREVKSVGLLVISGDRGLCGGYNTNVIRRAENRAKELKAEGLDYTFVI 119 Query: 118 IGSKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVN 177 +G K +FRI +GL , P +E +A+ + + + ++D + + Y +FV+ Sbjct: 120 VGRKAEQYFRRREQPIDASYTGLEQIPTADEANKIADELLSLFLSEKVDRIELVYTRFVS 179 Query: 178 TMSQKPVVQQLVPLP----ESKDDHL------NERQQTW------DYLYEPEP 214 +S +PV+Q L+PL E+ DD + ERQ Sbjct: 180 LVSSRPVIQTLLPLDTQGLEAADDEIFRLTTRGGQFQVERQTVTSQARPLPRDMIFEQDP 239 Query: 215 KVLLDSLLVRYLESQIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQAS 274 +LDSLL YL +Q+ +A+ ++ ASE AARM AM A++NAG LI L L YNKARQA+ Sbjct: 240 VQILDSLLPLYLSNQLLRALQESAASELAARMTAMSNASENAGELIKSLSLSYNKARQAA 299 Query: 275 ITNELNEIVAGAAAI 289 IT EL E+V GA A+ Sbjct: 300 ITQELLEVVGGAEAL 314 sp P41010 ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Bacillus 287 ATPG_BACCA caldotenax] AΑ align Score = 197 bits (500), Expect = 2e-49Identities = 118/290 (40%), Positives = 172/290 (58%), Gaps = 8/290 (2%) MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60 Query: 1 +A ++IKT+I + + T +ITKAMEMV+TSK+ + + RRPY E I+ V++ Sbjct: 4 LASLRDIKTRINATKKTSQITKAMEMVSTSKLNRAEKREIV-RPYMEKIQEVVA--MSAS 60 Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTL-NQIKNWKEQNISTDLGLIG 119 HP LV R VKK G LVI++DRG+ G N N+ + + KN Sbjct: 61 AARSHPMLVSRPVKKTGYLVITSDRGLAGAYNSNVVRLVYPKRSKNAMLPPDEIAIIVIG 120

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Query: 120 SKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTM 179
            G+SFFR + ++ L D P+ ++ +A ++G D +Y+ YN +V+ +
Sbjct: 121 RVGLSFFRKRNMPVILDITRLPDQPSFADIKEIARKTVGLFADGTFDELYMYYNHYVSAI 180
Query: 180 SQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVA 239
               ++L+PL D L E +Q Y +EP + +LD LL +Y ES IY A++D A
Sbjct: 181 QQEVTERKLLPLT----DFLAENKQRTVYEFEPSQEEILDVLLPQYAESLIYGALLDAKA 236
Query: 240 SEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
          SE AARM AMK ATDNA ++I L L YN+ARQA+IT E+ EIVAG A+
Sbjct: 237 SEHAARMTAMKNATDNANDVIRTLTLSYNRARQAAITQEITEIVAGRNAL 286
             ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Bacillus 287 AA
sp P42007
   ATPG_BACST stearothermophilus]
                                                                   align
 Score = 196 bits (499), Expect = 3e-49
 Identities = 121/292 (41%), Positives = 175/292 (59%), Gaps = 12/292 (4%)
Query: 1
          MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
          Sbjct: 4
          LASLRDIKTRINATKKTSQITKAMEMVSTSKLNRAAKREIV-RSYMEKIQEVVANV--AS 60
Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTD---LGL 117
           G HP LV R VKK G LVI++DRG+ G N N+ + L K K + D + +
Sbjct: 61 RGRSHPMLVSRPVKKTGYLVITSDRGLAGAYNSNVVR--LVYPKRSKNAMLPPDEYAIIV 118
Query: 118 IGSKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVN 177
          IG G+SFFR + ++ L D P+ ++ +A + +G D +Y+ YN +V+
Sbjct: 119 IGRVGLSFFRKRNMPVILDITRLPDQPSFADIKEIARKTVGLFADGTFDELYMYYNHYVS 178
Query: 178 TMSQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDN 237
         \cdot + Q+ ++L+PL D L E +Q Y +EP + +LD LL +Y ES IY A++D
Sbjct: 179 AIQQEVTERKLLPLT----DFLAENKQRTVYEFEPSQEEILDVLLPQYAESLIYGALLDA 234
Query: 238 VASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
           ASE AARM AMK ATDNA ++I L L YN+ARQA+IT E+ EIVAG A+
Sbjct: 235 KASEHAARMTAMKNATDNANDVIRTLTLSYNRARQAAITQEITEIVAGRNAL 286
tr Q927W3 AtpG protein [ATPG] [Listeria monocytogenes, Listeria innocua] 290 AA
                                                                      align
 Score = 195 bits (496), Expect = 6e-49
 Identities = 103/289 (35%), Positives = 168/289 (57%)
Query: 1
          MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
              +IK +I S + T +ITKAM+MV+ +K+ + + PY I++V++HV+
Sbjct: 1
         MASLIDIKQRITSTRKTSQITKAMQMVSAAKLGRAESNARSYEPYVSKIKDVVTHVASTG 60
Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
             HP LV R V + G +V+++D G+ G N ++ K +I + +G
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Sbjct:	61	${\tt NSSDHPMLVSRPVHRTGYIVLTSDTGLAGSYNSSVIKEVFQEINKKHTSSDEYAIITVGR}$	120
Query:	121	KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS FF++ N+ ++ G+ D P E+ +A+ + +G D V+I YN +N++S	180
Sbjct:	121	SARDFFKARQMNVVLEVQGITDHPIFAEIKDIASNTVQMFEDGVYDEVFIYYNHHINSIS	180
Query:	181	QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS + +QL+PL E + Y +EP + +L+ LL +Y+ES I+ A++D A+	240
Sbjct:	181	SELRKEQLLPLTEFHEKGKETDVDLTTYEFEPSEQEILEVLLPQYVESLIFGALLDAKAA	240
Query:	241	EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289 E AARM AM++ATDNA +LI+DL L YN+ARQA+IT E+ EIV GAAA+	
Sbjct:	241	EHAARMTAMRSATDNASDLISDLSLQYNRARQAAITQEITEIVGGAAAL 289	
		ATP synthase gamma chain, sodium ion specific (EC OMO 3.6.3.15) [ATPG] [Propionigenium modestum]	281 AA align
		194 bits (492), Expect = 2e-48 s = 109/289 (37%), Positives = 182/289 (62%), Gaps = 9/289 (3%	;)
Query:	2	AGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASI A KEIK++I+SVQST++ITKAME+V+++K +K Q + S+PYS ++ V+++++	61
Sbjct:	1	AAGKEIKSRISSVQSTRQITKAMEIVSSTKFKKFQALVNQSKPYSGSMDKVLANLAAGIK	60
Query:	62	GYKHP-FLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS +HP F + EVK+IGI+V+++DRG+CGG N + K I ++ +S IG	120
Sbjct:	61	NERHPLFDGKTEVKRIGIIVMTSDRGLCGGFNSSTLKEMEKLIVANPDKEVSVIAIGK	118
Query:	121	KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS KG + + + + K + L + + + + + + + D VY+ YN+F++ +S	180
Sbjct:	119	KGRDYCKKKDRDLKAEYIQLIPETMFDKAKEISENIVEYFYEDIFDEVYLIYNEFISALS	178
		QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS + +V++L+P+	
Sbjct:	179	TELIVKKLLPIERIEVQDNTTYIFEPSVEDILSSLLPKYLNIQLYQAILENTAS	232
Query:	241	EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289 E +AR AMK ATDNA ++I DL L YN+ RQA+IT E++EIV+GA+A+	
Sbjct:	233	EHSARKNAMKNATDNAEDMIKDLTLQYNRERQAAITQEISEIVSGASAL 281	
		ATP synthase gamma chain, chloroplast precursor (EC	370
ATP	G_PH	ATR 3.6.3.14) [ATPC] [Phaeodactylum tricornutum]	AA align
		194 bits (492), Expect = 2e-48 s = 114/313 (36%), Positives = 185/313 (58%), Gaps = 28/313 (8	୫)
Query:		AKEIKTKIASVQSTQKITKAMEMV-ATSKMRKTQDRMAASRPYSETIRNVISHVSKASIG A I+ +I SV++T+KIT AM++V A K+R+ QD + A+RP+SET+++V + + G	62
Sbjct:			117
Query:	63	YKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS	120

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P L EREVKK+ +LVI+ DRG+CGG N + K +
                                                   K+ + DL L+G
Sbjct: 118 ESVDLPLLTEREVKKVTLLVITGDRGLCGGYNSFMIKKAEARFNELKKNGVEADLILVGK 177
Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
          KGI++F GF I+ + G P ++ + + A + + +GE DAV + Y KFV+ ++
Sbjct: 178 KGIAYFERRGFPIRKKYE-TGQNPTAKQALAIAEEVSSTFLSGESDAVELLYTKFVSLIA 236
P ++ LVP S K D + +
Sbjct: 237 SSPSIRTLVPFSASDITAKGDEVFQLTSESGQFGVERTELDVAAPQEFPNDMIFEQDPIQ 296
Query: 217 LLDSLLVRYLESQIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASIT 276
          +++++L YL QI + + ++VASE AARM +M++A+DNAG+L L L YN+ARQA++T
Sbjct: 297 IVNAILPLYLNGQILRTLQESVASELAARMQSMQSASDNAGSLAKQLNLEYNRARQAAVT 356
Query: 277 NELNEIVAGAAAI 289
           EL EI++GA+A+
Sbjct: 357 QELLEIISGASAL 369
sp Q06908
             ATP synthase gamma chain, chloroplast precursor (EC
                                                                     370
   ATPG ODOSI 3.6.3.14)
                                                                     AA
              [ATPC] [Odontella sinensis (Marine centric diatom)]
                                                                     align
 Score = 194 bits (492), Expect = 2e-48
Identities = 111/312 (35%), Positives = 184/312 (58%), Gaps = 27/312 (8%)
          AKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIG- 62
          A I+ +I SV++T+KIT AM++VA +K+R+ QD + A+RP+SET+++V +
                                                              G
Sbjct: 59 ANAIRDRITSVKNTKKITMAMKLVAAAKVRRAQDAVLATRPFSETLQSVFGGLIARMGGE 118
Query: 63 -YKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSK 121
             P L +REV K+ ++VI+ DRG+CGG N + K + K+Q ++ D+ LIG K
Sbjct: 119 ALDLPLLTQREVSKVTLVVITGDRGLCGGYNSFMIKKAEARFNELKDQGVACDMVLIGKK 178
Query: 122 GISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMSO 181
          GI++F+ G+ I+ G P ++ + + + + Y +GE DAV + Y KF++ ++
Sbjct: 179 GITYFQRRGYPIRKTFE-TGQNPDSKQALAISEELLNTYLSGESDAVELLYTKFISLIAS 237
Query: 182 KPVVQQLVP------LPESKDDHLNERQQTW-----DYLYEPEPKVL 217
```

Query: 218 LDSLLVRYLESQIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITN 277 ++S+L YL QI + + ++VASE AARM +M++A+DNAG+L L YN+ARQA++T

LSDER+ Sbjct: 238 SPSARTLIPFSASEITQQGDEVFQLTSSGGDFEVERTELEVAEPQDFPNDMIFEQDPIQI 297

Sbjct: 298 INSILPLYLNGQILRTLQESVASELAARMQSMQSASDNAGDLAKRLSTEYNRARQAAVTQ 357

Query: 278 ELNEIVAGAAAI 289 E+ EIV+GA+A+

P + L+P

Sbjct: 358 EILEIVSGASAL 369

tr <u>Q8FQ21</u> H+-ATPase gamma subunit (EC 3.6.3.14) [ATPG] [Corynebacterium 326 AA efficiens]

align

tr	Q8KRI	J9 Subunit gamma [ATPG] [Ilyobacter tartaricus] 282 AA align	
		194 bits (492), Expect = 2e-48 s = 108/292 (36%), Positives = 181/292 (61%), Gaps = 13/292 (4	l %)
Query	: 1	MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS MAG KE+K +I SVQST +ITKAME+V+++K ++	60
Sbjct:	: 1	MAGGKELKGRIKSVQSTHQITKAMEIVSSTKFKRFSALVNPSKPYSKSMDRVLENIAAGI	60
Query	: 61	IGYKHP-FLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLI- KHP F +++VKKIG++V+++DRG+CGG N TL +++ +N ++ +1	118
Sbjct:	: 61	KSEKHPLFDGKKDVKKIGVIVMTSDRGLCGGFNNATLKKMEALIAENPGKEVSIIA	116
Query	: 119	-GSKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVN G K + +++K + L E+ ++ + D VY+ YN+FV+	177
Sbjct:	: 117	TGKKARDYCNKRNYDLKAEYIQLIPETMFEKAKEISENIVEYLHADIFDEVYMIYNEFVS	176
Query:	178	TMSQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDN M + V+++++P+	237
Sbjct:	: 177	AMQTELVMKRVLPIERVEAQENTTYIFEPSVEDILSSLLPKYLNIQIYQAILEN	230
Query:	238	VASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289 ASE +AR AMK ATDNA +I DL L YN+ RQA++T E++EIV+GA+A+	
Sbjct:	231	TASEHSARKNAMKNATDNAEEMIADLNLQYNRERQAAVTQEISEIVSGASAL 282	
sp <u>P4</u>	2/52	AMD	
AT		ATP synthase gamma chain (EC 3.6.3.14) [ATPG] THR [Enterococcus hirae]	300 AA align
Score	PG_EN	- · · · · · · · · · · · · · · · · · · ·	AA align
Score Ident	PG_EN	THR [Enterococcus hirae] 193 bits (490), Expect = 3e-48	AA align
Score Ident	PG_EN	THR [Enterococcus hirae] 193 bits (490), Expect = 3e-48 5 = 108/303 (35%), Positives = 179/303 (58%), Gaps = 21/303 (6 AGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVS	AA align 5%) 57
Score Ident Query: Sbjct:	PG_EN	THR [Enterococcus hirae] 193 bits (490), Expect = 3e-48 5 = 108/303 (35%), Positives = 179/303 (58%), Gaps = 21/303 (6 AGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVS A EIKT+IAS + T +IT+AM+MV+ SK+ K++ + Y+ +R +++H++	AA align 5%) 57 62
Score Ident Query: Sbjct: Query:	PG_EN e = 1 ities 2 3	THR [Enterococcus hirae] 193 bits (490), Expect = 3e-48 5 = 108/303 (35%), Positives = 179/303 (58%), Gaps = 21/303 (60) AGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVS A EIKT+IAS + T +IT+AM+MV+ SK+ K++ + Y+ +R +++H++ ASLNEIKTRIASTKKTSQITRAMQMVSASKLTKSEASSQKFQIYANKVREIVTHLTATQL KASIGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQ	AA align 5%) 57 62 109
Score Ident Query: Sbjct: Query: Sbjct:	PG_EN 2 = 1 3 = 58	THR [Enterococcus hirae] 193 bits (490), Expect = 3e-48 5 = 108/303 (35%), Positives = 179/303 (58%), Gaps = 21/303 (60) AGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVS A EIKT+IAS + T +IT+AM+MV+ SK+ K++ + Y+ +R +++H++ ASLNEIKTRIASTKKTSQITRAMQMVSASKLTKSEASSQKFQIYANKVREIVTHLTATQL KASIGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQ + I Y + L+ R VKK G +VI+ D G+ GG N ++ K T++ ++ +	AA align 5%) 57 62 109
Score Ident Query: Sbjct: Query: Sbjct:	PG_EN 2 = 1 58 = 58 63 = 110	THR [Enterococcus hirae] 193 bits (490), Expect = 3e-48 5 = 108/303 (35%), Positives = 179/303 (58%), Gaps = 21/303 (68) AGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVS A EIKT+IAS + T +IT+AM+MV+ SK+ K++ + Y+ +R +++H++ ASLNEIKTRIASTKKTSQITRAMQMVSASKLTKSEASSQKFQIYANKVREIVTHLTATQL KASIGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQ + I Y + L+ R VKK G +VI+ D G+ GG N ++ K T++ ++ NDIASDNPRGDINY-NSMLISRPVKKTGYIVITADGGLVGGYNSSILKQTMSILEEDHKS NISTDLGLIGSKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEID	AA align 5%) 57 62 109 121 166
Score Ident Query: Sbjct: Query: Query:	PG_EN e = 1 cities 2 3 58 63 110 122	THR [Enterococcus hirae] 193 bits (490), Expect = 3e-48 5 = 108/303 (35%), Positives = 179/303 (58%), Gaps = 21/303 (60) AGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVS A EIKT+IAS + T +IT+AM+MV+ SK+ K++ + Y+ +R +++H++ ASLNEIKTRIASTKKTSQITRAMQMVSASKLTKSEASSQKFQIYANKVREIVTHLTATQL KASIGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQ + I Y + L+ R VKK G +VI+ D G+ GG N ++ K T++ ++ NDIASDNPRGDINY-NSMLISRPVKKTGYIVITADGGLVGGYNSSILKQTMSILEEDHKS NISTDLGLIGSKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEID + IG G FF++ G N+ +L L D P+ +E ++G+A TM Y+N D	AA align 5%) 57 62 109 121 166 178
Score Ident Query: Sbjct: Query: Query: Sbjct: Query:	PG_EN e = 1 ities 2 3 58 63 110 122 167	THR [Enterococcus hirae] 193 bits (490), Expect = 3e-48 5 = 108/303 (35%), Positives = 179/303 (58%), Gaps = 21/303 (68) AGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVS A EIKT+IAS + T +IT+AM+MV+ SK+ K++ + Y+ +R ++++++ ASLNEIKTRIASTKKTSQITRAMQMVSASKLTKSEASSQKFQIYANKVREIVTHLTATQL KASIGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQ + I Y + L+ R VKK G +VI+ D G+ GG N ++ K T++ ++ + NDIASDNPRGDINY-NSMLISRPVKKTGYIVITADGGLVGGYNSSILKQTMSILEEDHKS NISTDLGLIGSKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEID + IG G FF++ G N+ +L L D P+ +E ++G+A TM Y+N D PDDYVMIAIGGTGADFFKARGINLAYELRNLSDQPSFDEVRKIVGMATTMYQNEVFD AVYIAYNKFVNTMSQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYL	AA align 5%) 57 62 109 121 166 178 226
Score Ident Query: Sbjct: Query: Sbjct: Query: Sbjct:	PG_EN e = 1 ities 2 3 58 63 110 122 167 179	THR [Enterococcus hirae] 193 bits (490), Expect = 3e-48 5 = 108/303 (35%), Positives = 179/303 (58%), Gaps = 21/303 (694) AGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVS A EIKT+IAS + T +IT+AM+MV+ SK+ K++ + Y+ +R +++H++ ASLNEIKTRIASTKKTSQITRAMQMVSASKLTKSEASSQKFQIYANKVREIVTHLTATQL	AA align (5%) (57) (62) (109) (121) (166) (178) (226) (236)
Score Ident Query: Sbjct: Query: Sbjct: Query: Sbjct: Query:	PG_EN e = 1 ities 2 3 58 63 110 122 167 179 227	THR [Enterococcus hirae] 193 bits (490), Expect = 3e-48 5 = 108/303 (35%), Positives = 179/303 (58%), Gaps = 21/303 (69) AGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVS A EIKT+IAS + T +IT+AM+MV+ SK+ K++ + Y+ +R ++++++ ASLNEIKTRIASTKKTSQITRAMQMVSASKLTKSEASSQKFQIYANKVREIVTHLTATQL KASIGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQ + I Y + L+ R VKK G +VI+ D G+ GG N ++ K T++ ++ + NDIASDNPRGDINY-NSMLISRPVKKTGYIVITADGGLVGGYNSSILKQTMSILEEDHKS NISTDLGLIGSKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEID + IG G FF++ G N+ +L L D P+ +E ++G+A TM Y+N D PDDYVMIAIGGTGADFFKARGINLAYELRNLSDQPSFDEVRKIVGMATTMYQNEVFD AVYIAYNKFVNTMSQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYL +Y+ YN +N+++ V++++P+ + Q +Y++EP + +L LL +Y ELYVCYNHHINSLTSQFRVEKMLPISDLDPEEATTFDQEYIFEPSKEEILAQLLPQYA	AA align (5%) (57) (62) (109) (121) (166) (178) (226) (236) (286)

+A+ Sbjct: 297 SAL 299

tr <u>Q8KAW9</u> ATP synthase F1, gamma subunit [ATPG] [Chlorobium tepidum] 292 AA align

Score = 192 bits (488), Expect = 5e-48Identities = 105/294 (35%), Positives = 181/294 (60%), Gaps = 9/294 (3%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60 M K+I+ ++ V+STQ++TKAM+MVA +K+R+ QDR +RPY+ ++ +++ +S

Sbjct: 1 MPTLKDIRIRLKGVKSTQQVTKAMKMVAAAKLRRAQDRAIQARPYAGKLKEMLASLSTKV 60

Query: 61 IGYKHPFLVERE-VKKIGILVISTDRGMCGGLNVNLFKTTLNQI-KNWKEQNISTDLGLI 118
+P L RE V + ++++++DRG+CGG N N+ K I + + + + + I

Sbjct: 61 DTSVNPLLSPREEVNNVLVILVTSDRGLCGGFNANIIKMAQRLIHEEYAALHAKGGVTMI 120

Query: 119 --GSKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFV 176
G+KG FFR G+ + G+ + + + +A+ Y +GE+D V + YN+F

Sbjct: 121 CAGTKGTEFFRKRGYKLAAAYPGVFQNLSFDSAREIADKASKMYLSGEVDRVVLVYNEFK 180

Query: 177 NTMSQKPVVQQLVPL-PESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVV 235
+ ++ +QL+P+ PE D + +YLYEP P ++D L+ ++L +O+++ ++

+ ++ +QL+P+ PE D + + +YLYEP P ++D L+ ++L +Q+++ ++ Sbjct: 181 SVLAPNLRTEQLLPITPEGGD----AKTASSEYLYEPSPAAIIDELVPKHLNTQLWRVML 236

22) 20. 101 2024 MERIDON INTRODUCTION OF ARTABOUT BEFORE THE MINISTER OF ARTABOUT BEFORE THE ARTABOUT BEFO

Query: 236 DNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289 ++ A+EQAARM AM +AT+NA LI L + YN+ARQA+IT EL+EIVAGA A+ Sbjct: 237 ESNAAEQAARMAAMDSATENAKELIRVLNISYNRARQAAITKELSEIVAGADAL 290

tr Q8RKV3 H+-ATPase cytoplasmic F1-part gamma-subunit [ATPG] [Streptococcus thermophilus]

292 AA align

Score = 192 bits (488), Expect = 5e-48 Identities = 107/292 (36%), Positives = 175/292 (59%), Gaps = 4/292 (1%)

Query: 1 MAGA-KEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKA 59
MAG+ +EIK KIAS++ T IT AM+MV+ SK+ +++ + Y+ IR + + + +

Sbjct: 1 MAGSLREIKAKIASIKQTSHITGAMQMVSASKLTRSEQAAKDFQIYASKIRQITTDLLHS 60

Query: 60 SI--GYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGL 117
+ G +P L R V+K G +VI++D+G+ GG N + K L+ IK + +

Sbjct: 61 ELVNGSSNPMLDARPVRKSGYIVITSDKGLVGGYNSTILKAVLDMIKRDHDSEDEYAIIS 120

Query: 118 IGSKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVN 177
IG G FF++ N+ +L GL D P+ +++ + + + Y+N D +Y+ YN +N

Sbjct: 121 IGGTGSDFFKARNMNVAFELRGLEDQPSFDQVGKIISKAVGMYQNELFDELYVCYNHHIN 180

Query: 178 TMSQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDN 237 ++S++ V++++P+ + D + +E + EP+ +LD LL +Y ES IY A+VD

Sbjct: 181 SLSREVRVEKMLPIADF-DPNESEGHVLTKFELEPDRDTILDQLLPQYAESLIYGAIVDA 239

Query: 238 VASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289 +E AA M AM+ ATDNA +INDL + YN+ARQA+IT E+ EIV GA+A+ Sbjct: 240 KTAEHAAGMTAMQTATDNAKKIINDLTIQYNRARQAAITQEITEIVGGASAL 291 ATP synthase gamma chain (EC 3.6.3.14) [ATPG] sp P08450 316 ATPG SYNP6 [Synechococcus sp. AA (strain PCC 6301) (Anacystis nidulans)] align Score = 191 bits (486), Expect = 8e-48 Identities = 111/315 (35%), Positives = 184/315 (58%), Gaps = 27/315 (8%) Query: 1 MAGAKEIKTKIASVOSTOKITKAMEMVATSKMRKTODRMAASRPYSETIRNVISHVSKAS 60 Sbjct: 1 MANLKAIRDRIKSVRNTRKITEAMRLVAAAKVRRAQEQVLSTRPFADRLAQVLAGLQQR- 59 Query: 61 IGYKH---PFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNOIKNWKEONISTDLGL 117 P L REVK + +LV+S DRG+CGG N N+ + + + 0 + Sbjct: 60 LQFENVDLPLLQRREVKTVALLVVSGDRGLCGGYNSNVIRRAEQRARELSAQGLDYKFVI 119 Query: 118 IGSKGISFFRSFGFNIKGOLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVN 177 +G K +F+ I+ SGL P +E +A+ + +G '+D V + Y KF++ Sbjct: 120 VGRKAGQYFQRREQPIEATYSGLEQIPTAQEANDIADELLSLFLSGTVDRVELVYTKFLS 179 Query: 178 TMSQKPVVQQLVPLPE----SKDDHLN------ERQQTW-----DYLYEPEP 214 ++ PVVQ L+PL S DD + ER++ Sbjct: 180 LVASNPVVQTLLPLDPQGLASSDDEIFRLTTRGGSFTVEREKLTSEVAPLPRDMIFEQDP 239 Query: 215 KVLLDSLLVRYLESQIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQAS 274 +L +LL YL +Q+ +A+ + ASE AARM AM +A+DNA L+ L LVYNKARQA+ Sbjct: 240 AQILSALLPLYLSNQLLRALQEAAASELAARMTAMNSASDNANALVGQLTLVYNKARQAA 299 Query: 275 ITNELNEIVAGAAAI 289 IT EL E+VAGA A+ Sbjct: 300 ITQELLEVVAGAEAL 314 sp Q05384 ATP synthase gamma chain (EC 3.6.3.14) [ATPG] 315 ATPG SYNP1 [Synechococcus sp. AΑ (strain PCC 6716)] align Score = 191 bits (484), Expect = 1e-47 Identities = 112/315 (35%), Positives = 181/315 (56%), Gaps = 27/315 (8%) Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60

```
Query: 178 TMSQKPVVQQLVPLP----ESKDD-------HLNERQQTW------DYLYEPEP 214
           +S KPVVQ L+PL E+ DD HL ++
                                                           D ++E +P
Sbjct: 180 LISSKPVVQTLLPLDPQGLEAADDEIFRLTTRASHLEVNREKVTSNLPALPPDMIFEQDP 239
Query: 215 KVLLDSLLVRYLESQIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQAS 274
            +LD+LL YL +O+ +A+ + ASE AARM AM A+DNA LI L L YNKAROA+
Sbjct: 240 VQILDALLPLYLSNQLLRALQEAAASELAARMTAMNNASDNAQTLIGTLTLSYNKARQAA 299
Query: 275 ITNELNEIVAGAAAI 289
          IT E+ E+VAGA A+
Sbjct: 300 ITQEILEVVAGAEAL 314
tr <u>Q8DLU1</u> H+-transporting ATP synthase gamma chain [ATPC] [Synechococcus 315 AA
          elongatus (Thermosynechococcus elongatus)]
                                                                      aliqn
 Score = 191 bits (484), Expect = 1e-47
 Identities = 111/315 (35%), Positives = 183/315 (57%), Gaps = 27/315 (8%)
Query: 1
          MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
          MA K I+ +I +++ T+KIT+AM +VA +K+R+ Q+++ ASRP+++ + V+ + +
Sbjct: 1
          MANLKAIRDRIKTIKDTRKITEAMRLVAAAKVRRAQEQVMASRPFADRLAQVLYSL-QTR 59
Query: 61 IGYKH---PFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGL 117
                 Sbjct: 60 LRFEDVDLPLLAKRPVKTVALLVVTGDRGLCGGYNTNVIRRAKERLQELEAEGLKYTLVI 119
Query: 118 IGSKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVN 177
          +G K +F+ + I SGL P+ E +A+ + + +D V + Y KFV+
Sbjct: 120 VGRKAAQYFQRRDYPIDAVYSGLEQIPSASEAGQIASELLSLFLSETVDRVELIYTKFVS 179
Query: 178 TMSQKPVVQQLVPLP----ESKDD-------HLNERQQ------TWDYLYEPEP 214
           +S KPVVQ L+PL E+ DD
                                          HL ++
Sbjct: 180 LISSKPVVQTLLPLDPQGLETADDEIFRLTTRGSHLEVNREKVTSTLPALPSDMIFEQDP 239
Query: 215 KVLLDSLLVRYLESQIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQAS 274
            +LD+LL YL +Q+ +A+ + ASE AARM AM A+DNA LI L L YNKAROA+
Sbjct: 240 LQILDALLPLYLNNQLLRALQEAAASELAARMTAMNNASDNAQALIGTLTLSYNKARQAA 299
Query: 275 ITNELNEIVAGAAAI 289
          IT E+ E+VAGA A+
Sbjct: 300 ITQEILEVVAGAEAL 314
sp P17253 ATP synthase gamma chain (EC 3.6.3.14) [ATPG]
                                                                       314
   ATPG_SYNY3 [Synechocystis sp.
                                                                      AΑ
              (strain PCC 6803)]
                                                                      align
Score = 190 bits (482), Expect = 2e-47
 Identities = 111/314 (35%), Positives = 182/314 (57%), Gaps = 25/314 (7%)
          MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSK-- 58
            K I+ +I SV++T+KIT+AM +VA +K+R+ Q+++ ++RP+++ + V+ ++
```

- Sbjct: 1 MPNLKAIRDRIQSVKNTKKITEAMRLVAAAKVRRAQEQVLSTRPFADALAOVLYNLONRL 60 Query: 59 ASIGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLI 118 + P +RE K + +LV++ DRG+CGG NVN K + K K O I+ L L+ Sbjct: 61 SFAETELPLFEQREPKAVALLVVTGDRGLCGGYNVNAIKRAEORAKELKNOGIAVKLVLV 120 Query: 119 GSKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNT 178 GSK +F +++ + L P E +A+++ + + +D V + Y +FV+ Sbjct: 121 GSKAKQYFGRRDYDVAASYANLEQIPNASEAAQIADSLVALFVSETVDRVELIYTRFVSL 180 Query: 179 MSQKPVVQQLVPLP----ESKDDHL------NERQQT------WDYLYEPEPK 215 +S +PVVQ L PL E+ DD + ER++ Sbjct: 181 ISSQPVVQTLFPLSPQGLEAPDDEIFRLITRGGKFQVEREKVEAPVESFPQDMIFEQDPV 240 Query: 216 VLLDSLLVRYLESQIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASI 275 +L++LL Y +Q+ +A+ ++ ASE AARM AM A+DNAG LI L L YNKARQA+I Sbjct: 241 QILEALLPLYNTNQLLRALQESAASELAARMTAMSNASDNAGQLIGTLTLSYNKARQAAI 300 Query: 276 TNELNEIVAGAAAI 289 T EL E+VAGA ++ Sbjct: 301 TQELLEVVAGANSL 314
- tr Q7NDC0 ATP synthase gamma chain [ATPC] [Gloeobacter 314 AA violaceus] align Score = 190 bits (482), Expect = 2e-47 Identities = 115/315 (36%), Positives = 190/315 (59%), Gaps = 28/315 (8%) Query: 1 MAGAKEIKTKIASVOSTOKITKAMEMVATSKMRKTODRMAASRPYSETIRNVISHVSKAS 60 M + I+ +I SV++TQKITKAM +VA +++R+ Q+++ A RP+++ + ++ ++ Sbjct: 1 MPNLRGIRDRIKSVKNTQKITKAMRLVAAARVRRAQEQVLAGRPFADRLVGLLFRL-RSR 59 Query: 61 IGYKH---PFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNOIKNWKEONISTDLGL 117 + ++ P + R+V+K+ +LVI+ DRG+CG N N+ + T+ ++ ++Q Sbjct: 60 LRFEDVQSPLMERRDVQKVLVLVIAGDRGLCGAYNSNIIRRTVQYLRELQQQGKQFALYL 119 Query: 118 IGSKGISFFRSFGFNIKGOLSGLGDTPALEELIG-VANTMFDAYRNGEIDAVYIAYNKFV 176 +G+K ISFFR F I L+ + LE + + + + +GE D V + Y +FV Sbjct: 120 VGNKAISFFRRSNFPIAKTLTNVDPNTPLEGANQLITDDILAPFLSGEYDQVELVYTRFV 179 Query: 177 NTMSQKPVVQQLVPL-PES--KDDH-------LNERQOTW------DYLYEPE 213 + +S +P VQ L+PL P++ ++D L E+QQ Sbjct: 180 SLISSRPTVQTLLPLDPDALGQEDETFKLITKGGGFEVLREKQQVRTEPEFAADTIFEQD 239 Query: 214 PKVLLDSLLVRYLESQIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQA 273 P LLD+LL YL S++ A+ ++ ASE AARM AM AA+DNA L++ L +VYNKARQA Sbjct: 240 PTQLLDALLPLYLTSEVLHALQESSASELAARMTAMSAASDNAKKLLSTLTIVYNKARQA 299 Query: 274 SITNELNEIVAGAAA 288 SIT E+ E+V+GA A Sbjct: 300 SITQEILEVVSGANA 314

299

AΑ

```
ATPG ACEWO 3.6.3.15)
               (Na(+)-translocating ATPase gamma chain) [ATPG]
                                                                         align
               [Acetobacterium woodii]
Score = 189 bits (480), Expect = 4e-47
 Identities = 111/298 (37%), Positives = 179/298 (59%), Gaps = 21/298 (7%)
Query: 5
          KEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYK 64
          ++IK +I SV ST +IT AME+VA++K+RK+++
                                                RPY E + I + S
Sbjct: 5
          QDIKPRIKSVNSTMQITHAMELVASAKLRKSRELAEGRRPYFEAMIESIGRIVEKSGNAR 64
Query: 65 HPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGIS 124
          + F+ +REVKK ++I+ D+G+ GG NVN+ K
                                                I + KE + L + GS + G
Sbjct: 65 NIFMDQREVKKTAYIIITGDKGLAGGYNVNVAKLVEEHITD-KENAV---LFTVGSRGRD 120
Ouery: 125 FFRSFGFNIKGOLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMSOKPV 184
                ++I+G+G+PV
                                        + + ++NGE D VYIAY KFV+T++Q
Sbjct: 121 HFRNREYHIQGEYLGISERPNFFNAKEVTAIVMEGFKNGEYDEVYIAYTKFVSTITQHAQ 180
Query: 185 VQQLVPLP-----ESKDDH--LNERQQTWDYLYEPEPKVLLDSLLVRYLES 228
                                E+K++
                                        +++R+ T
                                                   YEPEP+ LL L+
Sbjct: 181 MMKLLPLSREELITSGKVKTTEETKEEKSKMSDRELTI-MTYEPEPEELLKYLIPNLVSS 239
Query: 229 QIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGA 286
           +Y +++++ ASEQ AR AM++AT NA +I+ L L YN+ RQA IT E++EIV GA
Sbjct: 240 TVYGSMIESAASEQGARRTAMESATTNANEMIDGLTLQYNRVRQAPITQEISEIVGGA 297
tr Q7P5L4 ATP synthase gamma chain, sodium ion specific (EC 3.6.3.15) 282 AA
           [FNV0981] [Fusobacterium nucleatum subsp. vincentii ATCC
          49256]
                                                                      align
Score = 189 bits (480), Expect = 4e-47
Identities = 105/294 (35%), Positives = 178/294 (59%), Gaps = 17/294 (5%)
          MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
Query: 1
          M G KEIK++I SVQST++IT AME+V+T+K ++
                                              + SRPY +++R ++ +++
          MPGMKEIKSRIKSVQSTRQITNAMEIVSTTKFKRYSKLVTESRPYEKSMRKILGNIASGV 60
Sbjct: 1
Query: 61 IGYKHP-FLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLI- 118
                     +EVK I I+VI++DRG+CG N
                                                +TL +++
                                                         E+N + ++ +I
Sbjct: 61 KNEEHPLFDGRKEVKSIAIIVITSDRGLCGSFN----SSTLKELEKLVEKNRNKNITVIP 116
Query: 119 -GSKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVN 177
           GKIF
                      ++
                              S +
                                            ++ + + Y N
                                                         D VY+ YNKF++
Sbjct: 117 FGRKAIDFISKRNYDFSESFSKISPDEMNKIAGEISEEVVEKYNNHIYDEVYVIYNKFIS 176
Query: 178 TMSQKPVVQQLVPL--PESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVV 235
                  ++++P+ PES+
                                 LN
                                         +Y++EP + +L +LL R++ QIYQA++
```

Sbjct: 177 ALKYDLTCERIIPIARPESE---LNS----EYIFEPSAEYILSALLPRFINLQIYQAIL 228

+N ASE +AR +M +ATDNA +I L + YN+ RQ++IT E+ EIV GA+A+

Query: 236 DNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289

Sbjct: 229 NNTASEHSARKNSMSSATDNADEMIKTLNIKYNRNRQSAITQEITEIVGGASAL 282

```
Score = 189 \text{ bits } (479), Expect = 5e-47
 Identities = 98/286 (34%), Positives = 174/286 (60%), Gaps = 3/286 (1%)
          EIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHV--SKASIGY 63
Query: 6
          +IKTKIAS ++T +IT AM+MV+ +K+ ++++ + Y++ +R +++ +
          DIKTKIASTKNTSQITNAMQMVSAAKLGRSEEAARNFQVYAQKVRKLLTDILHGNGAGAS 66
Sbjct: 7
Query: 64 KHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGI 123
           +P L+ R VKK G +VI++DRG+ GG N ++ K + + +
Sbjct: 67 TNPMLISRSVKKTGYIVITSDRGLVGGYNSSILKAVMELKEEYHPDGKGFEMICIGGMGA 126
Query: 124 SFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMSQKP 183
                      +L GL D P+ +++ + + Y+N
                                                   D +Y+ YN VNT++ +
Sbjct: 127 DFFKARGIQPLYELRGLSDQPSFDQVRKIISKTVEMYQNELFDELYVCYNHHVNTLTSQM 186
Query: 184 VVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVASEQA 243
                      + +E + + + E + +L+ LL ++ ES IY A++D
           V+Q++P++
Sbjct: 187 RVEQMLPIVDLDPNEADE-EYSLTFELETSREEILEQLLPQFAESMIYGAIIDAKTAENA 245
Query: 244 ARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
          A M AM+ ATDNA +INDL + YN+ARQA+IT E+ EIVAGA+A+
Sbjct: 246 AGMTAMQTATDNAKKVINDLTIQYNRARQAAITQEITEIVAGASAL 291
```

tr Q8RGE1 ATP synthase gamma chain, sodium ion specific (EC 3.6.3.15) 282 AA [FN0359] [Fusobacterium nucleatum (subsp. nucleatum)]

align

```
Score = 187 bits (476), Expect = 1e-46
 Identities = 103/292 (35%), Positives = 174/292 (59%), Gaps = 13/292 (4%)
Query: 1
          MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
          M G KEIK++I SVQST++IT AME+V+T+K ++ + SRPY E++R ++ +++
Sbjct: 1
          MPGMKEIKSRIKSVQSTRQITNAMEIVSTTKFKRYSKLVTESRPYEESMRKILGNIASGV 60
Query: 61
          IGYKHP-FLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLI- 118
              HP F
                     +EVK I I+VI++DRG+CG N
                                               +TL +++
                                                         E+N + ++ +I
Sbjct: 61 KNEGHPLFDGRKEVKSIAIIVITSDRGLCGSFN----SSTLKELEKLVEKNKNKNITIIP 116
Query: 119 -GSKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVN 177
           GKIF
                     + S+
                                         ++ + + + Y N
                                                       D VY+ YNKF++
Sbjct: 117 FGRKAIDFITKRNYEFSESFSKISPDEMNKIAGEISEEVVEKYNNHIYDEVYVIYNKFIS 176
Query: 178 TMSQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDN 237
                  ++++P+ + + LN +Y++EP + +L R++ QIYQA+++N
Sbjct: 177 ALRYDLTCERIIPITRPEVE-LNS-----EYIFEPSTEYILSALLPRFINLQIYQAILNN 230
Query: 238 VASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
           ASE +AR +M +ATDNA +I L + YN+ RQ++IT E+ EIV GA+A+
Sbjct: 231 TASEHSARKNSMSSATDNADEMIKTLNIKYNRNRQSAITQEITEIVGGASAL 282
```

tr Q7MA19 ATP synthase F1 gamma subunit (EC 3.6.3.14) [ATPG] [Wolinella 298 AA succinogenes]

<u>4119</u>.

Score = 187 bits (475), Expect = 2e-46 Identities = 112/296 (37%), Positives = 168/296 (55%), Gaps = 15/296 (5%)

- Query: 5 KEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASI--- 61
 KEI+ KI SV++TQK TKAM++V+TSK++K ++ SR Y+E I V + KA I
- Sbjct: 6 KEIRKKITSVKNTQKTTKAMKLVSTSKLKKAEEMAKRSRVYAERITAVFQEI-KAKIEQN 64
- Query: 62 ---GYKHPFLV---EREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDL 115 G + P+ +REVK + I+ ++ D+G+CGG N K + +K QN+ L
- Sbjct: 65 GFSGLESPYFTAGEDREVKMVDIVFVTADKGLCGGFNSTTIKEVTRLMAEYKSQNVKVRL 124
- Query: 116 GLIGSKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKF 175

 IG KGISFF + ++S L TP E N + NG D V + +N F
- Sbjct: 125 RAIGKKGISFFGFNEVELLDKVSDLSATPDYERAAEFVNKATTDFINGVTDKVILVHNGF 184
- Query: 176 VNTMSQKPVVQQLVPLPESKDDHLNERQQTWDYLYEP--EPKVLLDSLLVRYLESQIYQA 233
 N +SQ+ VQ L+P+ K D + ++ EP + +LD L +Y+E +Y A
- Sbjct: 185 KNMISQELKVQDLLPI---KADAIEAKESLGMMEVEPSEQEREILDQLAKKYIEFNMYYA 241
- Query: 234 VVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289 ++D++A+E +ARM AM AA++NAG L+ L + YNKARQ +IT EL EI G ++
- Sbjct: 242 LIDSLAAEHSARMQAMDAASNNAGELVKSLTIAYNKARQEAITTELVEINTGVESM 297

tr Q9ZJ02 Proton-translocating ATPase gamma subunit [Streptococcus 293 sanguis] AA align

Score = 186 bits (473), Expect = 3e-46Identities = 102/287 (35%), Positives = 169/287 (58%), Gaps = 4/287 (1%)

- Query: 6 EIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVIS---HVSKASIG 62 +IK KIAS ++T +IT AM+MV+ +K+ K+++ + Y++ +R +++ H +A
- Sbjct: 7 DIKNKIASTKNTSQITNAMQMVSAAKLGKSEEAAKNFQVYAQKVRKLVTDMLHGHEAENA 66
- Query: 63 YKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKG 122
- Sbjct: 67 RHHSMLISRPVKKSAYIVITSDRGLVGGYNATILKALMELKAEYHPTGEDFEVICIGSVG 126
- Query: 123 ISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMSQK 182
- FFR+ G +L GL D P+ +E+ + + + Y+N D +Y+ YN VN+++ + Sbjct: 127 ADFFRARGIQPVYELRGLADQPSFDEVRKIISKTIEMYQNELFDELYVCYNHHVNSLTSQ 186
- Query: 183 PVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVASEQ 242
 - V+Q++P+ + + +E T + E +LD LL ++ ES IY A++D +E
- Sbjct: 187 MRVEQMLPIIDLDPNEADE-DYTLNLELESSRDSILDQLLPQFAESMIYGAIIDAKTAEN 245
- Query: 243 AARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
 AA M AM+ ATDNA +I+DL + YN+ARQA+IT E+ EIVAGA+A+

Sbjct: 246 AAGMTAMQTATDNAKKVISDLTIQYNRARQAAITQEITEIVAGASAL 292

tr <u>Q</u> 9FDR6	H+-ATPase gamma subunit (F0F1-type ATP synthase gamma subunit) (EC	AA
	3.6.1.34) [ATPG] [Corynebacterium glutamicum (Brevibacterium flavum)]	align
	186 bits (472), Expect = 4e-46 es = 112/319 (35%), Positives = 175/319 (54%), Gaps = 31/319 (9%)
		,
Query: 1	MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 6 MA +E++ +I SV ST+KITKA E++ATS++ K Q R+AA+ PY+E I+ V+ ++ AS	0
Sbjct: 1	MATIRELRDRIRSVNSTKKITKAQELIATSRITKAQGRVAAAAPYAEEIQRVLERLASAS 6	0
Query: 61	IGYKHPFLVEREV-KKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIG 1 HP L ERE K+ +LV+++DRGM GG N N+ K K E + G	19
Sbjct: 61	-SLDHPMLREREGGKRAAVLVVTSDRGMAGGYNHNVLKKAAELEKLLAESGYEVVRYVTG 1	19
Query: 12	SKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNG 1 KG+ +++ ++ G +G P V + D A+R G	63
Sbjct: 12) KKGVDYYKFRAEDVAGTWTGFSQDPDWAATHNVRRHLIDGFTASSEGEAAWREGLNLPEG 1	79
Query: 16	D V++ Y +F++ ++Q PVV QL+P+ +D + E+ + DY +	10
Sbjct: 18	QDIQGFDQVHVVYTEFISMLTQNPVVHQLLPVEPVIEDEIFEKGEDLLSSSGEVEPDYEF 2	39
Query: 21	EPEPKVLLDSLLVRYLESQIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKA 2 EP+ LL++LL +Y+ +++ ++ A+E A+R AMK+ATDNA L+ DL V N+A	70
Sbjct: 24	EPDADTLLEALLPQYVSRRLFSIFLEAAAAESASRRNAMKSATDNATELVKDLSRVANQA 2	99
Query: 27	RQASITNELNEIVAGAAAI 289 ROA IT E+ EIV GA A+	
Sbjct: 30	RQAQITQEITEIVGGAGAL 318	

flavum]	align
Score = 186 bits (472), Expect = 4e-46 Identities = 112/319 (35%), Positives = 175/319 (54%), Gaps = 31/319	(9%)
Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSK	
MA +E++ +I SV ST+KITKA E++ATS++ K Q R+AA+ PY+E I+ V+ ++ A Sbjct: 1 MATIRELRDRIRSVNSTKKITKAQELIATSRITKAQGRVAAAAPYAEEIQRVLERLASA	
Query: 61 IGYKHPFLVEREV-KKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGL HP L ERE K+ +LV+++DRGM GG N N+ K K E +	IG 119 G
Sbjct: 61 -SLDHPMLREREGGKRAAVLVVTSDRGMAGGYNHNVLKKAAELEKLLAESGYEVVRYV	_
Query: 120 SKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNG KG+ +++ ++ G +G P V + D A+R G	163
Sbjct: 120 KKGVDYYKFRAEDVAGAWTGFSQDPDWAATHNVRRHLIDGFTASSEGEAAWREGLNLP	EG 179
Query: 164EIDAVYIAYNKFVNTMSQKPVVQQLVPLPESKDDHLNERQQTWDY	LY 210

H+-ATPase gamma subunit [ATPG] [Brevibacterium

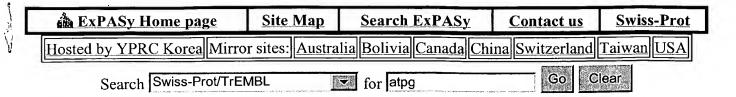
tr

325 AA

D V++ Y +F++ ++Q PVV QL+P+ +D + E+ + DY + Sbjct: 180 ODIOGFDOVHVVYTEFISMLTQNPVVHQLLPVEPVIEDEIFEKGEDLLSSSGEVEPDYEF 239 Query: 211 EPEPKVLLDSLLVRYLESQIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKA 270 EP+ LL++LL +Y+ +++ ++ A+E A+R AMK+ATDNA L+ DL V N+A Sbjct: 240 EPDADTLLEALLPQYVSRRLFSIFLEAAAAESASRRNAMKSATDNATELVKDLSRVANQA 299 Query: 271 RQASITNELNEIVAGAAAI 289 RQA IT E+ EIV GA A+ Sbjct: 300 RQAQITQEITEIVGGAGAL 318 trnew CAF19915 ATP SYNTHASE GAMMA SUBUNIT (EC 3.6.3.14) [ATPG] [Corynebacterium AΑ glutamicum (Brevibacterium flavum)] align Score = 186 bits (472), Expect = 4e-46 Identities = 112/319 (35%), Positives = 175/319 (54%), Gaps = 31/319 (9%) Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60 MA +E++ +I SV ST+KITKA E++ATS++ K Q R+AA+ PY+E I+ V+ ++ AS Sbjct: 1 MATIRELRDRIRSVNSTKKITKAQELIATSRITKAQGRVAAAAPYAEEIQRVLERLASAS 60 Query: 61 IGYKHPFLVEREV-KKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIG 119 HP L ERE K+ +LV+++DRGM GG N N+ K E Sbjct: 61 -SLDHPMLREREGGKRAAVLVVTSDRGMAGGYNHNVLKKAAELEKLLAESGYEVVRYVTG 119 Query: 120 SKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFD------AYRNG----- 163 KG+ +++ ++ G +G P V + D Sbjct: 120 KKGVDYYKFRAEDVAGTWTGFSQDPDWAATHNVRRHLIDGFTASSEGEAAWREGLNLPEG 179 Query: 164 ----EIDAVYIAYNKFVNTMSQKPVVQQLVPLPESKDDHLNERQQTW------DYLY 210 D V++ Y +F++ ++Q PVV QL+P+ +D + E+ + Sbjct: 180 QDIQGFDQVHVVYTEFISMLTQNPVVHQLLPVEPVIEDEIFEKGEDLLSSSGEVEPDYEF 239 Query: 211 EPEPKVLLDSLLVRYLESQIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKA 270 EP+ LL++LL +Y+ +++ ++ A+E A+R AMK+ATDNA L+ DL V N+A Sbjct: 240 EPDADTLLEALLPQYVSRRLFSIFLEAAAAESASRRNAMKSATDNATELVKDLSRVANQA 299 Query: 271 RQASITNELNEIVAGAAAI 289 RQA IT E+ EIV GA A+ Sbjct: 300 RQAQITQEITEIVGGAGAL 318 Database: EXPASY/UniProt Posted date: Mar 14, 2004 1:03 PM Number of letters in database: 451,237,162 Number of sequences in database: 1,414,857 Lambda K 0.316 0.131 0.358 Gapped Lambda K H 0.267 0.0410 0.140

Matrix: BLOSUM62 Gap Penalties: Existence: 11, Extension: 1 length of query: 289 length of database: 451,237,162 effective HSP length: 122 effective length of query: 167 effective length of database: 278,624,608 effective search space: 46530309536 effective search space used: 46530309536 T: 11 A: 40 X1: 16 (7.3 bits) X2: 38 (14.6 bits) X3: 64 (24.7 bits) S1: 41 (21.6 bits) S2: 72 (32.3 bits)

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Search in Swiss-Prot and TrEMBL for: atpg

Swiss-Prot Release 42.12 of 15-Mar-2004 TrEMBL Release 25.12 of 15-Mar-2004

- Number of sequences found in Swiss-Prot 68) and TrEMBL (132): 200
- Note that the selected sequences can be saved to a file to be later retrieved; to do so, go to the bottom of this page.
- For more directed searches, you can use the Sequence Retrieval System SRS.

Search in Swiss-Prot: There are matches to 68 out of 146193 entries

ATP6 STRMU (P95784)

ATP synthase a chain (EC 3.6.3.14) (ATPase protein 6). {GENE: ATPB OR ATPG OR SMU.1533} - Streptococcus mutans

ATPG ACEWO (**P50005**)

ATP synthase gamma chain, sodium ion specific (EC 3.6.3.15) (Na(+)-translocating ATP ase gamma chain). {GENE: ATPG OR UNCG} - Acetobacterium woodii

ATPG ANASP (P12408)

(ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR ATPC OR ALL0004} - Anabaena sp. (strain PCC 7120)

ATPG BACCA (P41010)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Bacillus caldotenax

ATPG BACHD (Q9K6H4)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR BH3755} - Bacillus halodurans ATPG BACME (**P20602**)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Bacillus megaterium ATPG BACP3 (**P09222**)

ATP synthase gamma chain precursor (EC 3.6.3.14). {GENE: ATPG} - Bacillus PS3 (Thermophilic bacterium PS-3)

ATPG BACPF (P22482)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Bacillus pseudofirmus ATPG BACST (P42007)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Bacillus stearothermophilus <u>ATPG BACSU (**P37810**)</u>

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR BSU36820} - Bacillus subtilis ATPG BOVIN (**P05631**)

ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14). {GENE: ATP5C} - Bos

tau

taurus (Bovine)

ATPG_BUCAI (P57123)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR BU007} - Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum symbiotic bacterium)

<u>ATPG_BUCAP</u> (**O51873**)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR BUSG007} - Buchnera aphidicola (subsp. Schizaphis graminum)

ATPG BUCBP (Q89B40)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR BBP007} - Buchnera aphidicola (subsp. Baizongia pistaciae)

ATPG CHLRE (P12113)

ATP synthase gamma chain, chloroplast precursor (EC 3.6.3.14). {GENE: ATPC} - Chlamydomonas reinhardtii

ATPG_DROME (**001666**)

ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14). {GENE: ATPSYN-GAMMA OR CG7610} - Drosophila melanogaster (Fruit fly)

ATPG ECOLI (P00837)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR UNCG OR PAPC OR B3733 OR C4659 OR Z5231 OR ECS4675 OR SF3813 OR S3955} - Escherichia coli, Escherichia coli O6, Escherichia coli O157:H7, Shigella flexneri

ATPG ENTHR (P43452)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Enterococcus hirae

ATPG HAEIN (P43716)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR HI0480} - Haemophilus influenzae

ATPG HELPJ (Q9ZK80)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR JHP1061} - Helicobacter pylori J99 (Campylobacter pylori J99)

ATPG HELPY (P56082)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR HP1133} - Helicobacter pylori (Campylobacter pylori)

ATPG HUMAN (**P36542**)

ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14). {GENE: ATP5C1 OR ATP5C} - Homo sapiens (Human)

ATPG KLULA (P49377)

ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14). {GENE: ATP3 OR MGI5} - Kluyveromyces lactis (Yeast)

ATPG LACLA (Q9CER9)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR LL1765} - Lactococcus lactis (subsp. lactis) (Streptococcus lactis)

ATPG_METMA (Q60189)

V-type ATP synthase subunit G-(EC 3.6.3.14) (V-type ATPase subunit G). {GENE: ATPG OR AHAG OR MM0777.1} - Methanosarcina mazei (Methanosarcina frisia)

ATPG MOUSE (Q91VR2)

ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14). {GENE: ATP5C1} - Mus musculus (Mouse)

ATPG MYCGA (P33257)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR MYCGA3050 OR MGA_1174} - Mycoplasma gallisepticum

<u>ATPG MYCGE (**P47640**)</u>

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR MG400} - Mycoplasma

genitalium

ATPG MYCLE (P45824)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR ML1144} - Mycobacterium leprae ATPG MYCPN (Q50330)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR MPN599 OR MP243} - Mycoplasma pneumoniae

ATPG MYCTU (Q10597)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR RV1309 OR MT1349 OR MTCY373.29 OR MB1341} - Mycobacterium tuberculosis, Mycobacterium bovis

ATPG ODOSI (**Q06908**)

ATP synthase gamma chain, chloroplast precursor (EC 3.6.3.14). {GENE: ATPC} - Odontella sinensis (Marine centric diatom)

ATPG PASMU (Q9L6B6)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR PM1493} - Pasteurella multocida ATPG PEA (P28552)

ATP synthase gamma chain, chloroplast precursor (EC 3.6.3.14). {GENE: ATPC} - Pisum sativum (Garden pea)

<u>ATPG PHATR</u> (**Q41075**)

ATP synthase gamma chain, chloroplast precursor (EC 3.6.3.14). {GENE: ATPC} - Phaeodactylum tricornutum

<u>ATPG_PROMO</u> (**P29710**)

ATP synthase gamma chain, sodium ion specific (EC 3.6.3.15). {GENE: ATPG OR UNCG} - Propionigenium modestum

ATPG RAT (**P35435**)

ATP synthase gamma chain, mitochondrial (EC 3.6.3.14). {GENE: ATP5C} - Rattus norvegicus (Rat)

ATPG_RHOBL (**P05436**)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Rhodopseudomonas blastica

ATPG RHOCA (P72246)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Rhodobacter capsulatus (Rhodopseudomonas capsulata)

ATPG RHORU (P07227)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Rhodospirillum rubrum ATPG RICPR (**O50289**)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR RP802} - Rickettsia prowazekii ATPG SCHPO (**074754**)

ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14). {GENE: ATP3 OR SPBC1734.13} - Schizosaccharomyces pombe (Fission yeast)

<u>ATPG_SPIOL</u> (**P05435**)

ATP synthase gamma chain, chloroplast precursor (EC 3.6.3.14). {GENE: ATPC} - Spinacia oleracea (Spinach)

ATPG_SPIPL (**P50006**)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR ATPC} - Spirulina platensis ATPG STRLI (**P50007**)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Streptomyces lividans

ATPG_STRMU (**P95788**)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR ATPC OR SMU.1529} - Streptococcus mutans

ATPG SYNP1 (Q05384)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR ATPC} - Synechococcus sp. (strain PCC 6716)

ATPG SYNP6 (P08450)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR ATPC} - Synechococcus sp. (strain PCC 6301) (Anacystis nidulans)

ATPG SYNY3 (P17253)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR ATPC OR SLL1327} -Synechocystis sp. (strain PCC 6803)

ATPG THIFE (**P41169**)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Thiobacillus ferrooxidans

ATPG TOBAC (**P29790**)

ATP synthase gamma chain, chloroplast precursor (EC 3.6.3.14). {GENE: ATPC} - Nicotiana tabacum (Common tobacco)

ATPG_VIBAL (**P12990**)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR UNCG} - Vibrio alginolyticus

ATPG YEAST (**P38077**)

ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14). {GENE: ATP3 OR YBR039W OR YBR0408} - Saccharomyces cerevisiae (Baker's yeast)

ATPX_ANASP (P12410)
ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG OR ALL0008} - Anabaena sp. (strain PCC 7120)

ATPX ANTSP (Q02852)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - Antithamnion sp

ATPX CYACA (Q9TM29)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - Cyanidium caldarium

ATPX CYAPA (**P48085**)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - Cyanophora paradoxa

ATPX GALSU (P35012)_

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - Galdieria sulphuraria (Red alga)

ATPX GUITH (**078478**)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - Guillardia theta (Cryptomonas phi)

<u>ATPX OCHNE</u> (**Q40608**)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - Ochrosphaera neapolitana ATPX ODOSI (**Q00823**)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - Odontella sinensis (Marine centric diatom)

ATPX PORPU (P51245)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - Porphyra purpurea

ATPX RHORU (P15015) =-

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - Rhodospirillum rubrum ATPX SPIOL (P31853)

ATP synthase B' chain, chloroplast precursor (EC 3.6.3.14) (Subunit II). {GENE: ATPG} -Spinacia oleracea (Spinach)

ATPX SYNP1 (Q05367)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - Synechococcus sp. (strain PCC 6716)

ATPX SYNP6 (P08446)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - Synechococcus sp. (strain PCC 6301) (Anacystis nidulans)

ATPX SYNY3 (**P27183**)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG OR SLL1323} - Synechocystis



sp. (strain PCC 6803)

VATD SULTO (P22721)

V-type ATP synthase subunit D (EC 3.6.3.14) (V-type ATPase subunit D) (Sul-ATPase gamma chain). {GENE: ATPD OR ATPG OR ST1438} - Sulfolobus tokodaii, Sulfolobus acidocaldarius

Search in TrEMBL: There are matches to 132 out of 1070786 entries

O05432

ATP synthase subunit gamma {GENE:ATPG} - Moorella thermoacetica (Clostridium thermoaceticum)

O31083

ATP synthase gamma subunit N-terminus homolog {GENE:ATPG} - Methanosarcina barkeri O50141

Proton-translocating ATPase, gamma subunit {GENE:ATPG} - Ruminococcus albus O50158

Proton-translocating ATPase, gamma-subunit {GENE:ATPG} - Streptococcus bovis O66581

ATP synthase £1 gamma subunit {GENE:ATPG2 OR AQ_203} - Aquifex aeolicus O67829

ATP synthase F1 gamma subunit {GENE:ATPG1 OR AQ_2041} - Aquifex aeolicus O42139

H+-transporting ATP synthase CHAIN9 - like protein (AT4G32260/F10M6_100) {GENE:ATPG OR F10M6.100 OR AT4G32260} - Arabidopsis thaliana (Mouse-ear cress)

Q7MA19

ATP synthase F1 gamma subunit (EC 3.6.3.14) {GENE:ATPG OR WS0515} - Wolinella succinogenes

Q7NA93

ATP synthase gamma chain {GENE:ATPG OR PLU0041} - Photorhabdus luminescens (subsp. laumondii)

Q7NCS0

ATP synthase b' chain of CF(0) {GENE:ATPG OR GLL2908} - Gloeobacter violaceus Q7P096

H+-transporting two-sector ATPase, gamma subunit (EC 3.6.3.14) {GENE:ATPG OR CV0671} - Chromobacterium violaceum

Q7U8W8

Putative ATP synthase subunit B' (EC 3.6.3.14) {GENE:ATPG OR SYNW0491} - Synechococcus sp. (strain WH8102)

Q7UFB6

ATP synthase gamma subunit (EC 3.6.1.34) {GENE:ATPG OR RB10216} - Rhodopirellula baltica

Q7UH04

ATP synthase gamma subunit C-terminus homolog (EC 3.6.1.34) {GENE:ATPG OR RB4917} - Rhodopirellula baltica

O7V034

ATP synthase B/B' CF(0) (EC 3.6.3.14) {GENE:ATPG OR PMM1454} - Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4)

Q7V5S4

ATP synthase B/B' CF(0) precursor (EC 3.6.3.14) {GENE:ATPG OR PMT1470} - Prochlorococcus marinus (strain MIT 9313)

O7VA64

ATP synthase gamma chain {GENE:ATPG OR PRO1603} - Prochlorococcus marinus

FoF1-type ATP synthase (EC 3.6.3.14) {GENE:ATPG OR HH0428} - Helicobacter hepaticus O7VPP1

ATP synthase gamma chain {GENE:ATPG OR HD0009} - Haemophilus ducreyi

Q7VQV7

ATP synthase gamma subunit (EC 3.6.3.14) {GENE:ATPG OR BFL007} - Candidatus Blochmannia floridanus

Q7VU45

ATP synthase gamma chain (EC 3.6.3.14) {GENE:ATPG OR PAPC OR UNCG OR BP3287} - Bordetella pertussis

Q7W3A9

ATP synthase gamma chain (EC 3.6.3.14) {GENE:ATPG OR PAPC OR UNCG OR BPP4136} - Bordetella parapertussis

O7WEM8

ATP synthase gamma chain (EC 3.6.3.14) {GENE:ATPG OR PAPC OR UNCG OR BB4606} - Bordetella bronchiseptica (Alcaligenes bronchisepticus)

Q7XZD7

Hypothetical protein atpG (Fragment) {GENE:ATPG} - Drosera tokaiensis

Q7XZD8

Hypothetical protein atpG (Fragment) {GENE:ATPG} - Drosera tokaiensis

Q81JZ4

ATP synthase F1, gamma subunit {GENE:ATPG OR BA5548} - Bacillus anthracis (strain Ames) O82J83

Putative ATP synthase gamma chain {GENE:ATPG OR SAV2882} - Streptomyces avermitilis Q82XP9

ATP synthase gamma subunit (EC 3.6.3.14) {GENE:ATPG OR NE0205} - Nitrosomonas europaea

Q831A4

ATP synthase F1, gamma subunit {GENE:ATPG OR EF2609} - Enterococcus faecalis (Streptococcus faecalis)

Q83AF6

ATP synthase, F1 gamma subunit {GENE:ATPG OR CBU1944} - Coxiella burnetii Q83G90

ATP synthase gamma chain (EC 3.6.1.34) {GENE:ATPG OR TWT425} - Tropheryma whipplei (strain Twist) (Whipple's bacillus)

Q83HY1

ATP synthase gamma chain (EC 3.6.3.14) {GENE:ATPG OR TW343} - Tropheryma whipplei (strain TW08/27) (Whipple's bacillus)

Q83U82

ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - Haemophilus influenzae O83U83

ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - Haemophilus influenzae Q83UA6

ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - Haemophilus influenzae O83V83

ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - Haemophilus influenzae Q83V84

ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - Haemophilus influenzae Q83V85

ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - Haemophilus influenzae Q83V86

ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - Haemophilus influenzae Q83V87

ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - Haemophilus influenzae Q83V88

ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - Haemophilus influenzae O83V89

ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - Haemophilus influenzae 084DX7

ATP synthase F1 complex gamma chain (Fragment) {GENE:ATPG} - Tropheryma whipplei (Whipple's bacillus) (Tropheryma whippelii)

Q85FR1

ATP synthase CF0 B' chain (Subunit II) {GENE:ATPG} - Cyanidioschyzon merolae (Red alga) [Chloroplast]

Q87E89

ATP synthase gamma chain {GENE:ATPG OR PD0429} - Xylella fastidiosa (strain Temecula1 / ATCC 700964)

Q87TT3

ATP synthase £1, gamma subunit {GENE:ATPG OR PSPTO5600} - Pseudomonas syringae (pv. tomato)

Q88BX3

ATP synthase F1, gamma subunit (GENE: ATPG OR PP5414) - Pseudomonas putida (strain KT2440)

O88UU2

H(+)-transporting two-sector ATPase, gamma subunit (EC 3.6.3.14) {GENE:ATPG OR LP_2365} - Lactobacillus plantarum

O89X73

ATP synthase gamma chain {GENE:ATPG OR BLL0441} - Bradyrhizobium japonicum Q8D3J4

AtpG protein {GENE:ATPG OR WIGBR0070} - Wigglesworthia glossinidia brevipalpis Q8DLP6

H+-transporting ATP synthase chain b' {GENE:ATPG OR TLR0432} - Synechococcus elongatus (Thermosynechococcus elongatus)

Q8E073

ATP synthase F1, gamma subunit {GENE:ATPG OR SAG0862} - Streptococcus agalactiae (serotype V)

Q8E5U9

H+-transporting ATP synthase gamma chain {GENE:ATPG OR GBS0880} - Streptococcus agalactiae (serotype III)

Q8E8B9

ATP synthase F1, gamma subunit {GENE:ATPG OR SO4748} - Shewanella oneidensis Q8EM82

H(+)-transporting ATP synthase gamma chain (EC 3.6.1.34) {GENE:ATPG OR OB2976} - Oceanobacillus iheyensis

Q8F2J4

ATP synthase F1, gamma subunit (EC 3.6.1.34) {GENE:ATPG OR LA2778} - Leptospira interrogans

Q8FQ21

H+-ATPase gamma subunit (ÈC 3.6.3.14) {GENE:ATPG OR CE1314} - Corynebacterium efficiens



Q8FYR4

ATP synthase F1, gamma subunit {GENE:ATPG OR BR1800} - Brucella suis O8G7B2

ATP synthaşe gamma chain {GENE:ATPG OR BL0358} - Bifidobacterium longum

Q8KAW9
ATP synthase F1, gamma subunit {GENE:ATPG OR CT2032} - Chlorobium tepidum

Q8KM29

F1F0-ATPase subunit gamma {GENE:ATPG} - Oenococcus oeni (Leuconostoc oenos) Q8KRU9

Subunit_gamma {GENE:ATPG} - Ilyobacter tartaricus

Q8PCZ6

ATP synthase gamma chain {GENE:ATPG OR XCC0553} - Xanthomonas campestris (pv. campestris)

Q8PGG6

ATP synthase gamma chain {GENE:ATPG OR XAC3650} - Xanthomonas axonopodis (pv. citri) O8RC16

F0F1-type ATP synthase gamma subunit {GENE:ATPG OR TTE0636} - Thermoanaerobacter tengcongensis

Q8RKV3

H+-ATPase cytoplasmic F1-part gamma-subunit {GENE:ATPG} - Streptococcus thermophilus Q8UC75

ATP synthase gamma chain {GENE:ATPG OR ATU2623 OR AGR_C_4756} - Agrobacterium tumefaciens (strain C58 / ATCC 33970)

Q8VL83

ATP synthase F1, subunit gamma (Fragment) {GENE:ATPG} - Helicobacter pylori (Campylobacter pylori)

Q8VV78

F0F1-ATPase subunit gamma {GENE:ATPG} - Colwellia maris (Vibrio sp. (strain ABE-1)) Q8XID3

ATP synthase gamma subunit {GENE:ATPG OR CPE2188} - Clostridium perfringens Q8XU75

Probable ATP synthase gamma chain protein (EC 3.6.1.34) {GENE:ATPG OR RSC3318 OR RS02548} - Ralstonia solanacearum (Pseudomonas solanacearum)

Q8Z2Q5

ATP synthase gamma subunit-{GENE:STY3912 OR ATPG OR T3653} - Salmonella typhi Q8Z9S5

ATP synthase gamma subunit protein (ÈC 3.6.1.34) (Membrane-bound ATP synthase, F1 sector, gamma-subunit) {GENE:ATPG OR YPO4122 OR Y4136} - Yersinia pestis

Q8ZKW8

Membrane-bound ATP synthase, F1 sector, gamma-subunit (EC 3.6.3.14) {GENE:ATPG OR STM3866} - Salmonella typhimurium

Q927W3

AtpG protein {GENE:ATPG OR LMO2530 OR LIN2674} - Listeria monocytogenes, Listeria innocua

Q92G87

ATP synthase gamma chain {GENE:ATPG OR RC1236} - Rickettsia conorii

Q92LK7

Probable ATP synthase gamma chain protein (EC 3.6.1.34) {GENE:ATPG OR R03035 OR SMC02500} - Rhizobium meliloti (Sinorhizobium meliloti)

Q92VG5

Putative ATRGTP-binding protein {GENE:RB0740 OR SMB21236} - Rhizobium meliloti



(Sinorhizobium meliloti) [Plasmid pSymB (megaplasmid 2)] O92VY6

Putative ATPGTP-binding hydroxymethyltransferase protein {GENE:RB0561 OR SMB20821} - Rhizobium meliloti (Sinorhizobium meliloti) [Plasmid pSymB (megaplasmid 2)]

O93Q45

ATP synthase gamma subunit {GENE:ATPG} - Clostridium pasteurianum O93U19

ATP synthase gamma-subunit {GENE:ATPG} - Carsonella ruddii Q93U22

ATP synthase gamma-subunit {GENE:ATPG} - Carsonella ruddii O93U62

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii O93U65

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii O93U68

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii Q93U71

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii O93U74

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii Q93U77

ATP synthase gamma subunit $\{GENE:ATPG\}$ - Carsonella ruddii O93U80

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii Q93U83

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii Q93U86

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii O93U89

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii O93U92

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii Q93U95

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii O93U98

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii Q93UA1

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii O93UA4

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii Q93UA7

ATP synthase gamma subunit $\{GENE:ATPG\}$ - Carsonella ruddii O93UB0

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii Q93UB3

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii O93UB6

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii Q93UB9

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii Q93UC2

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii O93UC5

ATP synthase gamma subunit (GENE:ATPG) - Carsonella ruddii

Q93UC8

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii Q93UD1

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii Q93UD7

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii

Q93UE0

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii Q93UE3

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii Q97PT5

ATP synthase F1, gamma subunit (Proton-translocating ATPase gamma subunit) (Proton-translocating ATPase, F1 sector, gamma-subunit) (EC 3.6.1.34) {GENE:SP1509 OR ATPG OR SPR1361} - Streptococcus pneumoniae, Streptococcus pneumoniae (strain ATCC BAA-255 / R6) O97ZR2

ATP synthase subunit G (atpG) (EC 3.6.1.34) {GENE:ATPG OR SSO6175} - Sulfolobus solfataricus

Q99SF4

ATP synthase gamma chain {GENE:ATPG OR SAV2104 OR SA1906 OR MW2028} - Staphylococcus aureus (strain Mu50 / ATCC 700699), Staphylococcus aureus (strain N315), Staphylococcus aureus (strain MW2)

Q9A0I8

Putative proton-translocating ATPase, gamma subunit (EC 3.6.1.34) {GENE:ATPG OR SPY0759 OR SPYM18_0817} - Streptococcus pyogenes, Streptococcus pyogenes (serotype M18)

Q9AHX1

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii

<u>Q9FAA4</u>

H+-ATPase gamma subunit {GENE:ATPG} - Brevibacterium flavum

Q9FDR6

H+-ATPase gamma subunit (F0F1-type ATP synthase gamma subunit) (EC 3.6.1.34) {GENE:ATPG OR CGL1211} - Corynebacterium glutamicum (Brevibacterium flavum)

Q9HT19

ATP synthase gamma chain {GENE:ATPG OR PA5555} - Pseudomonas aeruginosa W71

ATP synthase gamma chain (EC 3.6.1.34) {GENE:ATPG OR NMA0518} - Neisseria meningitidis (serogroup A)

O9K4D4

ATP synthase gamma chain-{GENE:ATPG OR SCO5372 OR 2SC6G5.16} - Streptomyces coelicolor

Q9PJ20

ATP synthase F1 sector gamma subunit (EC 3.6.1.34) {GENE:ATPG OR CJ0106} - Campylobacter jejuni $_{\odot}$

O9PR14

ATP synthase gamma chain {GENE:ATPG OR UU130} - Ureaplasma parvum (Ureaplasma urealyticum biotype 1)

Q9RAU1



H+-ATPase cytoplasmic F1-part gamma-subunit (H+-ATPase gamma subunit) {GENE:ATPG} - Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris), Lactococcus lactis (subsp. lactis) (Streptococcus lactis)

O9RFL4

ATP synthase subunit gamma $\{GENE:ATPG\}$ - Salmonella typhimurium Q9RGY2

F1F0-ATPase subunit gamma {GENE:ATPG} - Lactobacillus acidophilus

Gamma subunit of membrane-bound ATP synthase $\{GENE:ATPG\}$ - Buchnera aphidicola O9RO77

Gamma subunit of membrane-bound ATP synthase $\{GENE:ATPG\}$ - Buchnera aphidicola O9RO80

Gamma subunit of membrane-bound ATP synthase $\{GENE:ATPG\}$ - Buchnera aphidicola O9S5B6

F1F0-ATPase gamma subunit {GENE:ATPG} - Desulfovibrio vulgaris O9SBM3

CFO ATP synthase subunit II {GENE:ATPG} - Volvox carteri f. nagariensis Q9Z688

ATP synthase subunit gamma (FOF1-type ATP synthase gamma subunit) {GENE:ATPG OR CAC2866} - Clostridium acetobutylicum Q9ZR72

P-glycoprotein {GENE:ATPGP1 OR T1J8.9} - Arabidopsis thaliana (Mouse-ear cress)

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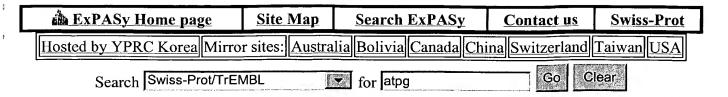
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ATP6 STRMU (P95784)

ATP synthase a chain (EC 3.6.3.14) (ATPase protein 6). {GENE: ATPB OR ATPG OR SMU.1533} - Streptococcus mutans

ATPG ACEWO (P50005)

ATP synthase gamma chain, sodium ion specific (EC 3.6.3.15) (Na(+)-translocating ATPase gamma chain). {GENE: ATPG OR UNCG} - Acetobacterium woodii

ATPG ANASP (P12408)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR ATPC OR ALL0004} - Anabaena sp. (strain PCC 7120)

ATPG BACCA (P41010)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Bacillus caldotenax

ATPG BACHD (Q9K6H4)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR BH3755} - Bacillus halodurans ATPG_BACME (**P20602**)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Bacillus megaterium

ATPG BACP3 (P09222)

ATP synthase gamma chain precursor (EC 3.6.3.14). {GENE: ATPG} - Bacillus PS3 (Thermophilic bacterium PS-3)

<u>ATPG BACPF</u> (**P22482**)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Bacillus pseudofirmus ATPG BACST (P42007)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Bacillus stearothermophilus ATPG BACSU (P37810)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR BSU36820} - Bacillus subtilis <u>ATPG_BOVIN</u> (**P05631**)

ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14). {GENE: ATP5C} - Bos

taurus (Bovine)

ATPG BUCAI (P57123)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR BU007} - Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum symbiotic bacterium)

<u>ATPG BUCAP</u> (**051873**)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR BUSG007} - Buchnera aphidicola (subsp. Schizaphis graminum)

ATPG BUCBP (Q89B40)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR BBP007} - Buchnera aphidicola (subsp. Baizongia pistaciae)

ATPG CHLRE (P12113)

ATP synthase gamma chain, chloroplast precursor (EC 3.6.3.14). {GENE: ATPC} - Chlamydomonas reinhardtii

ATPG DROME (O01666)

ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14). {GENE: ATPSYN-GAMMA OR CG7610} - Drosophila melanogaster (Fruit fly)

ATPG ECOLI (P00837)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR UNCG OR PAPC OR B3733 OR C4659 OR Z5231 OR ECS4675 OR SF3813 OR S3955} - Escherichia coli, Escherichia coli O6, Escherichia coli O157:H7, Shigella flexneri

ATPG ENTHR (P43452)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Enterococcus hirae

ATPG HAEIN (P43716)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR HI0480} - Haemophilus influenzae

ATPG HELPJ (Q9ZK80)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR JHP1061} - Helicobacter pylori J99 (Campylobacter pylori J99)

ATPG HELPY (P56082)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR HP1133} - Helicobacter pylori (Campylobacter pylori)

ATPG HUMAN (P36542)

ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14). {GENE: ATP5C1 OR ATP5C} - Homo sapiens (Human)

ATPG KLULA (P49377)

ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14). {GENE: ATP3 OR MGI5} - Kluyveromyces lactis (Yeast)

ATPG LACLA (**Q9CER9**)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR LL1765} - Lactococcus lactis (subsp. lactis) (Streptococcus lactis)

ATPG METMA (**Q60189**)

V-type ATP synthase subunit G (EC 3.6.3.14) (V-type ATPase subunit G). {GENE: ATPG OR AHAG OR MM0777.1} - Methanosarcina mazei (Methanosarcina frisia)

ATPG MOUSE (Q91VR2)

ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14). {GENE: ATP5C1} - Mus musculus (Mouse)

ATPG MYCGA (P33257)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR MYCGA3050 OR MGA_1174} - Mycoplasma gallisepticum

ATPG MYCGE (P47640)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR MG400} - Mycoplasma

genitalium

ATPG MYCLE (P45824)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR ML1144} - Mycobacterium leprae ATPG MYCPN (Q50330)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR MPN599 OR MP243} - Mycoplasma pneumoniae

ATPG_MYCTU (Q10597)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR RV1309 OR MT1349 OR MTCY373.29 OR MB1341} - Mycobacterium tuberculosis, Mycobacterium bovis

ATPG ODOSI (Q06908)

ATP synthase gamma chain, chloroplast precursor (EC 3.6.3.14). {GENE: ATPC} - Odontella sinensis (Marine centric diatom)

ATPG PASMU (Q9L6B6)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR PM1493} - Pasteurella multocida ATPG PEA (**P28552**)

ATP synthase gamma chain, chloroplast precursor (EC 3.6.3.14). {GENE: ATPC} - Pisum sativum (Garden pea)

ATPG PHATR (Q41075)

ATP synthase gamma chain, chloroplast precursor (EC 3.6.3.14). {GENE: ATPC} - Phaeodactylum tricornutum

<u>ATPG_PROMO</u> (**P29710**)

ATP synthase gamma chain, sodium ion specific (EC 3.6.3.15). {GENE: ATPG OR UNCG} - Propionigenium modestum

ATPG RAT (**P35435**)

ATP synthase gamma chain, mitochondrial (EC 3.6.3.14). {GENE: ATP5C} - Rattus norvegicus (Rat)

ATPG RHOBL (P05436)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Rhodopseudomonas blastica

<u>ATPG_RHOCA</u> (**P72246**)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Rhodobacter capsulatus (Rhodopseudomonas capsulata)

ATPG RHORU (P07227)

ATP synthase gamma chain (EC 3.6.3.14). $\{GENE: ATPG\}$ - Rhodospirillum rubrum

<u>ATPG_RICPR</u> (**O50289**)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR RP802} - Rickettsia prowazekii ATPG SCHPO (**074754**)

ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14). {GENE: ATP3 OR SPBC1734.13} - Schizosaccharomyces pombe (Fission yeast)

ATPG SPIOL (P05435)

ATP synthase gamma chain, chloroplast precursor (EC 3.6.3.14). {GENE: ATPC} - Spinacia oleracea (Spinach)

ATPG SPIPL (P50006)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR ATPC} - Spirulina platensis ATPG STRLI (**P50007**)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Streptomyces lividans

ATPG_STRMU (P95788)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR ATPC OR SMU.1529} - Streptococcus mutans

ATPG SYNP1 (**Q05384**)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR ATPC} - Synechococcus sp. (strain PCC 6716)

ATPG SYNP6 (P08450)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR ATPC} - Synechococcus sp. (strain PCC 6301) (Anacystis nidulans)

ATPG SYNY3 (P17253)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR ATPC OR SLL1327} - Synechocystis sp. (strain PCC 6803)

ATPG THIFE (P41169)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Thiobacillus ferrooxidans ATPG TOBAC (**P29790**)

ATP synthase gamma chain, chloroplast precursor (EC 3.6.3.14). {GENE: ATPC} - Nicotiana tabacum (Common tobacco)

ATPG VIBAL (P12990)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR UNCG} - Vibrio alginolyticus ATPG YEAST (P38077)

ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14). {GENE: ATP3 OR YBR039W OR YBR0408} - Saccharomyces cerevisiae (Baker's yeast)

<u>ATPX_ANASP</u> (P12410)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG OR ALL0008} - Anabaena sp. (strain PCC 7120)

<u>ATPX ANTSP</u> (Q02852)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - Antithamnion sp

ATPX CYACA (Q9TM29)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - Cyanidium caldarium

<u>ATPX_CYAPA</u> (**P48085**)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - Cyanophora paradoxa ATPX GALSU (**P35012**)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - Galdieria sulphuraria (Red alga)

ATPX GUITH (078478)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - Guillardia theta (Cryptomonas phi)

ATPX OCHNE (Q40608)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - Ochrosphaera neapolitana ATPX ODOSI (**Q00823**)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - Odontella sinensis (Marine centric diatom)

ATPX_PORPU (P51245)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - Porphyra purpurea ATPX RHORU (P15015)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - Rhodospirillum rubrum ATPX SPIOL (**P31853**)

ATP synthase B' chain, chloroplast precursor (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - Spinacia oleracea (Spinach)

ATPX SYNP1 (Q05367)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - Synechococcus sp. (strain PCC 6716)

ATPX SYNP6 (P08446)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - Synechococcus sp. (strain PCC 6301) (Anacystis nidulans)

ATPX SYNY3 (**P27183**)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG OR SLL1323} - Synechocystis

sp. (strain PCC 6803)

VATD SULTO (P22721)

V-type ATP synthase subunit D (EC 3.6.3.14) (V-type ATPase subunit D) (Sul-ATPase gamma chain). {GENE: ATPD OR ATPG OR ST1438} - Sulfolobus tokodaii, Sulfolobus acidocaldarius

Search in TrEMBL: There are matches to 132 out of 1070786 entries

O05432

ATP synthase subunit gamma {GENE:ATPG} - Moorella thermoacetica (Clostridium thermoaceticum)

O31083

ATP synthase gamma subunit N-terminus homolog $\{GENE:ATPG\}$ - Methanosarcina barkeri O50141

Proton-translocating ATPase, gamma subunit {GENE:ATPG} - Ruminococcus albus O50158

Proton-translocating ATPase, gamma subunit {GENE:ATPG} - Streptococcus bovis O66581

ATP synthase F1 gamma subunit {GENE:ATPG2 OR AQ_203} - Aquifex aeolicus O67829

ATP synthase F1 gamma subunit {GENE:ATPG1 OR AQ_2041} - Aquifex aeolicus Q42139

H+-transporting ATP synthase CHAIN9 - like protein (AT4G32260/F10M6_100) {GENE:ATPG OR F10M6.100 OR AT4G32260} - Arabidopsis thaliana (Mouse-ear cress)

Q7MA19

ATP synthase F1 gamma subunit (EC 3.6.3.14) {GENE:ATPG OR WS0515} - Wolinella succinogenes

Q7NA93

ATP synthase gamma chain {GENE:ATPG OR PLU0041} - Photorhabdus luminescens (subsp. laumondii)

Q7NCS0

ATP synthase b' chain of CF(0) {GENE:ATPG OR GLL2908} - Gloeobacter violaceus O7P096

H+-transporting two-sector ATPase, gamma subunit (EC 3.6.3.14) {GENE:ATPG OR CV0671} - Chromobacterium violaceum

Q7U8W8

Putative ATP synthase subunit B' (EC 3.6.3.14) {GENE:ATPG OR SYNW0491} - Synechococcus sp. (strain WH8102)

Q7UFB6

ATP synthase gamma subunit (EC 3.6.1.34) {GENE:ATPG OR RB10216} - Rhodopirellula baltica

Q7UH04

ATP synthase gamma subunit C-terminus homolog (EC 3.6.1.34) {GENE:ATPG OR RB4917} - Rhodopirellula baltica

O7V034

ATP synthase B/B' CF(0) (EC 3.6.3.14) {GENE:ATPG OR PMM1454} - Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4)

Q7V5S4

ATP synthase B/B' CF(0) precursor (EC 3.6.3.14) {GENE:ATPG OR PMT1470} - Prochlorococcus marinus (strain MIT 9313)

Q7VA64

ATP synthase gamma chain {GENE:ATPG OR PRO1603} - Prochlorococcus marinus O7VJ22

FoF1-type ATP synthase (EC 3.6.3.14) {GENE:ATPG OR HH0428} - Helicobacter hepaticus Q7VPP1

ATP synthase gamma chain {GENE:ATPG OR HD0009} - Haemophilus ducreyi Q7VQV7

ATP synthase gamma subunit (EC 3.6.3.14) {GENE:ATPG OR BFL007} - Candidatus Blochmannia floridanus

Q7VU45

ATP synthase gamma chain (EC 3.6.3.14) {GENE:ATPG OR PAPC OR UNCG OR BP3287} - Bordetella pertussis

Q7W3A9

ATP synthase gamma chain (EC 3.6.3.14) {GENE:ATPG OR PAPC OR UNCG OR BPP4136} - Bordetella parapertussis

Q7WEM8

ATP synthase gamma chain (EC 3.6.3.14) {GENE:ATPG OR PAPC OR UNCG OR BB4606} - Bordetella bronchiseptica (Alcaligenes bronchisepticus)

Q7XZD7

Hypothetical protein atpG (Fragment) {GENE:ATPG} - Drosera tokaiensis

Q7XZD8

Hypothetical protein atpG (Fragment) {GENE:ATPG} - Drosera tokaiensis

Q81JZ4

ATP synthase F1, gamma subunit {GENE:ATPG OR BA5548} - Bacillus anthracis (strain Ames) <u>Q82J83</u>

Putative ATP synthase gamma chain {GENE:ATPG OR SAV2882} - Streptomyces avermitilis Q82XP9

ATP synthase gamma subunit (EC 3.6.3.14) {GENE:ATPG OR NE0205} - Nitrosomonas europaea

Q831A4

ATP synthase F1, gamma subunit {GENE:ATPG OR EF2609} - Enterococcus faecalis (Streptococcus faecalis)

Q83AF6

ATP synthase, F1 gamma subunit {GENE:ATPG OR CBU1944} - Coxiella burnetii Q83G90

ATP synthase gamma chain (EC 3.6.1.34) {GENE:ATPG OR TWT425} - Tropheryma whipplei (strain Twist) (Whipple's bacillus)

Q83HY1

ATP synthase gamma chain (EC 3.6.3.14) {GENE:ATPG OR TW343} - Tropheryma whipplei (strain TW08/27) (Whipple's bacillus)

Q83U82

ATP synthase F1 epsilon subunit (Fragment) $\{GENE:ATPG\}$ - Haemophilus influenzae $\underline{Q83U83}$

ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - Haemophilus influenzae Q83UA6

ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - Haemophilus influenzae Q83V83

ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - Haemophilus influenzae Q83V84

ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - Haemophilus influenzae Q83V85

ATP synthase F1 epsilon subunit (Fragment) $\{GENE:ATPG\}$ - Haemophilus influenzae O83V86

ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - Haemophilus influenzae Q83V87

ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - Haemophilus influenzae O83V88

ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - Haemophilus influenzae O83V89

ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - Haemophilus influenzae Q84DX7

ATP synthase F1 complex gamma chain (Fragment) {GENE:ATPG} - Tropheryma whipplei (Whipple's bacillus) (Tropheryma whippelii)

Q85FR1

ATP synthase CF0 B' chain (Subunit II) {GENE:ATPG} - Cyanidioschyzon merolae (Red alga) [Chloroplast]

O87E89

ATP synthase gamma chain {GENE:ATPG OR PD0429} - Xylella fastidiosa (strain Temecula1 / ATCC 700964).

Q87TT3

ATP synthase F1, gamma subunit {GENE:ATPG OR PSPTO5600} - Pseudomonas syringae (pv. tomato)

Q88BX3

ATP synthase F1, gamma subunit {GENE:ATPG OR PP5414} - Pseudomonas putida (strain KT2440)

Q88UU2

H(+)-transporting two-sector ATPase, gamma subunit (EC 3.6.3.14) {GENE:ATPG OR LP_2365} - Lactobacillus plantarum

O89X73

ATP synthase gamma chain {GENE:ATPG OR BLL0441} - Bradyrhizobium japonicum Q8D3J4

AtpG protein {GENE:ATPG OR WIGBR0070} - Wigglesworthia glossinidia brevipalpis Q8DLP6

H+-transporting ATP synthase chain b' {GENE:ATPG OR TLR0432} - Synechococcus elongatus (Thermosynechococcus elongatus)

Q8E073

ATP synthase F1, gamma subunit {GENE:ATPG OR SAG0862} - Streptococcus agalactiae (serotype V)

Q8E5U9

H+-transporting ATP synthase gamma chain $\{GENE:ATPG\ OR\ GBS0880\}$ - Streptococcus agalactiae (serotype III)

Q8E8B9

ATP synthase F1, gamma subunit {GENE:ATPG OR SO4748} - Shewanella oneidensis Q8EM82

H(+)-transporting ATP synthase gamma chain (EC 3.6.1.34) {GENE:ATPG OR OB2976} - Oceanobacillus iheyensis

Q8F2J4

ATP synthase F1, gamma subunit (EC 3.6.1.34) {GENE:ATPG OR LA2778} - Leptospira interrogans

Q8FQ21

H+-ATPase gamma subunit (EC 3.6.3.14) {GENE:ATPG OR CE1314} - Corynebacterium efficiens

Q8FYR4

ATP synthase F1, gamma subunit {GENE:ATPG OR BR1800} - Brucella suis

Q8G7B2

ATP synthase gamma chain {GENE:ATPG OR BL0358} - Bifidobacterium longum O8KAW9

ATP synthase F1, gamma subunit {GENE:ATPG OR CT2032} - Chlorobium tepidum Q8KM29

F1F0-ATPase subunit gamma {GENE:ATPG} - Oenococcus oeni (Leuconostoc oenos) Q8KRU9

Subunit gamma {GENE:ATPG} - Ilyobacter tartaricus

Q8PCZ6

ATP synthase gamma chain {GENE:ATPG OR XCC0553} - Xanthomonas campestris (pv. campestris)

Q8PGG6

ATP synthase gamma chain {GENE:ATPG OR XAC3650} - Xanthomonas axonopodis (pv. citri) Q8RC16

F0F1-type ATP synthase gamma subunit {GENE:ATPG OR TTE0636} - Thermoanaerobacter tengcongensis

Q8RKV3

H+-ATPase cytoplasmic F1-part gamma-subunit {GENE:ATPG} - Streptococcus thermophilus Q8UC75

ATP synthase gamma chain {GENE:ATPG OR ATU2623 OR AGR_C_4756} - Agrobacterium tumefaciens (strain C58 / ATCC 33970)

Q8VL83

ATP synthase F1, subunit gamma (Fragment) {GENE:ATPG} - Helicobacter pylori (Campylobacter pylori)

Q8VV78

F0F1-ATPase subunit gamma {GENE:ATPG} - Colwellia maris (Vibrio sp. (strain ABE-1)) Q8XID3

ATP synthase gamma subunit {GENE:ATPG OR CPE2188} - Clostridium perfringens Q8XU75

Probable ATP synthase gamma chain protein (EC 3.6.1.34) {GENE:ATPG OR RSC3318 OR RS02548} - Ralstonia solanacearum (Pseudomonas solanacearum)

Q8Z2Q5

ATP synthase gamma subunit {GENE:STY3912 OR ATPG OR T3653} - Salmonella typhi Q8Z9S5

ATP synthase gamma subunit protein (EC 3.6.1.34) (Membrane-bound ATP synthase, F1 sector, gamma-subunit) {GENE:ATPG OR YPO4122 OR Y4136} - Yersinia pestis

Q8ZKW8

Membrane-bound ATP synthase, F1 sector, gamma-subunit (EC 3.6.3.14) {GENE:ATPG OR STM3866} - Salmonella typhimurium

O927W3

AtpG protein {GENE:ATPG OR LMO2530 OR LIN2674} - Listeria monocytogenes, Listeria innocua

Q92G87

ATP synthase gamma chain {GENE:ATPG OR RC1236} - Rickettsia conorii

O92LK7

Probable ATP synthase gamma chain protein (EC 3.6.1.34) {GENE:ATPG OR R03035 OR SMC02500} - Rhizobium meliloti (Sinorhizobium meliloti)

Q92VG5

Putative ATPGTP-binding protein {GENE:RB0740 OR SMB21236} - Rhizobium meliloti

(Sinorhizobium meliloti) [Plasmid pSymB (megaplasmid 2)] O92VY6

Putative ATPGTP-binding hydroxymethyltransferase protein {GENE:RB0561 OR SMB20821} - Rhizobium meliloti (Sinorhizobium meliloti) [Plasmid pSymB (megaplasmid 2)]

Q93Q45

ATP synthase gamma subunit $\{GENE:ATPG\}$ - Clostridium pasteurianum O93U19

ATP synthase gamma-subunit {GENE:ATPG} - Carsonella ruddii Q93U22

ATP synthase gamma-subunit $\{GENE:ATPG\}$ - Carsonella ruddii O93U62

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii Q93U65

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii Q93U68

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii Q93U71

ATP synthase gamma subunit $\{GENE:ATPG\}$ - Carsonella ruddii O93U74

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii Q93U77

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii Q93U80

ATP synthase gamma subunit $\{GENE:ATPG\}$ - Carsonella ruddii O93U83

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii Q93U86

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii Q93U89

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii Q93U92

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii Q93U95

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii O93U98

ATP synthase gamma subunit $\{GENE:ATPG\}$ - Carsonella ruddii O93UA1

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii O93UA4

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii Q93UA7

ATP synthase gamma subunit $\{GENE:ATPG\}$ - Carsonella ruddii O93UB0

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii O93UB3

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii O93UB6

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii Q93UB9

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii O93UC2

ATP synthase gamma subunit $\{GENE:ATPG\}$ - Carsonella ruddii O93UC5

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii $093\underline{UC8}$

ATP synthase gamma subunit $\{GENE:ATPG\}$ - Carsonella ruddii O93UD1

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii

ATP synthase gamma subunit $\{GENE:ATPG\}$ - Carsonella ruddii O93UD7

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii O93UE0

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii Q93UE3

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii O97PT5

ATP synthase F1, gamma subunit (Proton-translocating ATPase gamma subunit) (Proton-translocating ATPase, F1 sector, gamma-subunit) (EC 3.6.1.34) {GENE:SP1509 OR ATPG OR SPR1361} - Streptococcus pneumoniae, Streptococcus pneumoniae (strain ATCC BAA-255 / R6) O97ZR2

ATP synthase subunit G (atpG) (EC 3.6.1.34) {GENE:ATPG OR SSO6175} - Sulfolobus solfataricus

Q99SF4

ATP synthase gamma chain {GENE:ATPG OR SAV2104 OR SA1906 OR MW2028} - Staphylococcus aureus (strain Mu50 / ATCC 700699), Staphylococcus aureus (strain N315), Staphylococcus aureus (strain MW2)

O9A018

Putative proton-translocating ATPase, gamma subunit (EC 3.6.1.34) {GENE:ATPG OR SPY0759 OR SPYM18_0817} - Streptococcus pyogenes, Streptococcus pyogenes (serotype M18)

Q9AHX1

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii

<u>Q9FAA4</u>

H+-ATPase gamma subunit {GENE:ATPG} - Brevibacterium flavum

O9FDR6

H+-ATPase gamma subunit (F0F1-type ATP synthase gamma subunit) (EC 3.6.1.34) {GENE:ATPG OR CGL1211} - Corynebacterium glutamicum (Brevibacterium flavum) Q9HT19

ATP synthase gamma chain {GENE:ATPG OR PA5555} - Pseudomonas aeruginosa Q9JW71

ATP synthase gamma chain (EC 3.6.1.34) {GENE:ATPG OR NMA0518} - Neisseria meningitidis (serogroup A)

O9K4D4

ATP synthase gamma chain {GENE:ATPG OR SCO5372 OR 2SC6G5.16} - Streptomyces coelicolor

O9PJ20

ATP synthase F1 sector gamma subunit (EC 3.6.1.34) {GENE:ATPG OR CJ0106} - Campylobacter jejuni

Q9PR14

ATP synthase gamma chain {GENE:ATPG OR UU130} - Ureaplasma parvum (Ureaplasma urealyticum biotype 1)

Q9RAU1

H+-ATPase cytoplasmic F1-part gamma-subunit (H+-ATPase gamma subunit) {GENE:ATPG} - Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris), Lactococcus lactis (subsp. lactis) (Streptococcus lactis)

O9RFL4

ATP synthase subunit gamma {GENE:ATPG} - Salmonella typhimurium O9RGY2

F1F0-ATPase subunit gamma {GENE:ATPG} - Lactobacillus acidophilus

Gamma subunit of membrane-bound ATP synthase {GENE:ATPG} - Buchnera aphidicola O9RO77

Gamma subunit of membrane-bound ATP synthase $\{GENE:ATPG\}$ - Buchnera aphidicola O9RO80

Gamma subunit of membrane-bound ATP synthase $\{GENE:ATPG\}$ - Buchnera aphidicola O9S5B6

F1F0-ATPase gamma subunit {GENE:ATPG} - Desulfovibrio vulgaris

CFO ATP synthase subunit II {GENE:ATPG} - Volvox carteri f. nagariensis O9Z688

ATP synthase subunit gamma (FOF1-type ATP synthase gamma subunit) {GENE:ATPG OR CAC2866} - Clostridium acetobutylicum O9ZR72

P-glycoprotein {GENE:ATPGP1 OR T1J8.9} - Arabidopsis thaliana (Mouse-ear cress)

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L1: Entry 72 of 74

File: DWPI

Aug 11, 2003

DERWENT-ACC-NO: 1998-011056

DERWENT-WEEK: 200408

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TITLE: Bacteria from the family <u>Pasteurellaceae</u> producing repeat in toxin (RTX) - in in non-activated form, useful for preparing live attenuated vaccines against (Haemophilus, Actinobacilus and Pasteurella

Basic Abstract Text (1):

Bacteria from the family Pasteurellaceae producing 'repeat in toxin' (RTX) in a nonactivated form are new.

Basic Abstract Text (2):

USE - The bacteria are useful for preparing live attentuated vaccines for protecting animals against infection by an RTX-producing bacterium of the family Pasteurellaceae, especially Actinobacillus pleuropneumoniae or Pasteurella haemolytica (claimed).

Actinobacillus actinomycefemeomitans
Actinobacillus suis
Actinobacillus pleuropneumoniais
Pasteurella anatipestiter
Pasteurella haemolytica
Pasteurella muttocida
Haemophitus parasuis
Influenzas
Somnus
Somnus
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L1: Entry 70 of 74

File: DWPI

Mar 26, 2003

DERWENT-ACC-NO: 2000-647422

DERWENT-WEEK: 200327

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TITLE: Attenuated <u>Pasteurellaceae</u> bacteria comprising mutations in virulence genes, useful as a live attenuated vaccine against bacterial infections

Basic Abstract—Text (T):

NOVELTY - A gram negative bacteria, such as attenuated Pasteurellaceae, comprising a mutation in a virulence gene, selected from one of 68 defined sequences (N1-N68) (given in the specification), is new.

Basic Abstract Text (4):

(2) a method for producing a gram-negative bacteria mutant, such as attenuated Pasteurellaceae, comprising introducing a mutation into any of N1 to N68, resulting in decreased activity of a gene product encoded by the mutated gene;

Basic Abstract Text (5):

(3) a purified and isolated <u>Pasteurellaceae</u> polynucleotide comprising a nucleotide sequence selected from one of N1 to N68 or sequences which hybridize to them;

PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION International Bureau



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 7:		(11) International Publication Number: WO 00/61724
C12N 1/21, C07K 14/285, A61K 35/74, 39/02, C12N 15/63, 15/31, C07K 16/12, C12Q 1/18	A2	(43) International Publication Date: 19 October 2000 (19.10.00)
(21) International Application Number: PCT/US (22) International Filing Date: 6 April 2000 (c) (30) Priority-Data: 60/128,689 9 April 1999 (09.04.99) 60/153,453 10 September 1999 (10.09.9) (71) Applicant: PHARMACIA & UPJOHN, INC. [US/Henrictta Street, Kalamazoo, MI 49001 (US). (72) Inventors: LOWERY, David, E.; 1207 Woodlan Portage, MI 49024 (US). FULLER, Troy, E.; 11 field Drive, Battle Creek, MI 49014 (US). KE Michael, J.; 2364 Quincy Avenue, Portage, MI 490 (74) Agent: WILLIAMS, Joseph, A., Jr.; Marshall, Gerstein, Murray & Borun, 6300 Sears Tower, 2 Wacker Drive, Chicago, IL 60606–6402 (US).	06.04.0 9) - U US]; 30 d Driv I Drear NNED 024 (US	BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Te, Published Without international search report and to be republished upon receipt of that report.
(57) Abstract Gram negative bacterial virulence genes are identified these virulence genes and their products, and the provision	ed, the	reby allowing the identification of novel anti-bacterial agents that target rel gram negative bacterial mutants useful in vaccines.

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1. Document ID: ZA 200108262 A, WO 200061724 A2, AU 200040776 A, EP 1171577 A2, BR 200009663 A, KR 2001112937 A, CN 1351653 A, JP 2002541790 W

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L4: Entry 1 of 1

File: DWPI

Mar 26, 2003

DERWENT-ACC-NO: 2000-647422

DERWENT-WEEK: 200327

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TITLE: Attenuated <u>Pasteurellaceae</u> bacteria comprising mutations in virulence genes, useful as a live attenuated vaccine against bacterial infections

INVENTOR: FULLER, T E; KENNEDY, M J ; LOWERY, D E

PRIORITY-DATA: 1999US-153453P (September 10, 1999), 1999US-128689P (April 9, 1999)

PATENT-FAMILY:

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
ZA 200108262 A	March-26, 2003		337	C12N000/00
WO 200061724 A2	October 19, 2000	E	320	C12N001/21
AU 200040776 A	November 14, 2000		000	C12N001/21
EP 1171577 A2	January 16, 2002	E	000	C12N001/21
BR 200009663 A	April 9, 2002		000	C12N001/21
KR 2001112937 A	December 22, 2001		000	C12N001/21
CN 1351653 A	May 29, 2002		000	C12N001/21
JP 2002541790 W	December 10, 2002		341	C12N015/09

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L4: Entry 1 of 1

File: DWPI

Mar 26, 2003

DERWENT-ACC-NO: 2000-647422

DERWENT-WEEK: 200327

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TITLE: Attenuated <u>Pasteurellaceae</u> bacteria comprising mutations in virulence genes, useful as a live attenuated vaccine against bacterial infections

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Basic Abstract Text (4):

(2) a method for producing a gram-negative bacteria mutant, such as attenuated Pasteurellaceae, comprising introducing a mutation into any of N1 to N68, resulting in decreased activity of a gene product encoded by the mutated gene;

Basic Abstract Text (5):

(3) a purified and isolated <u>Pasteurellaceae</u> polynucleotide comprising a nucleotide sequence selected from one of N1 to N68 or sequences which hybridize to them;

Basic Abstract Text (16):

Nine groups of pigs were used to determine the safety and efficacy of seven A. pleuropneumoniae mutants as live attenuated vaccine strains. Seven groups were infected intranasally with 1010 colony forming units (CFU) of each mutant on day 1. One group was vaccinated on days 1 and 15 with the commercially available vaccine Pleuromune (Bayer), and one naive group was not vaccinated. On day 29, all groups were challenged intranasally with 1-5 multiply 105 CFU per pig of wild type APP225. All surviving animals were euthanized and necropsied on day 42 of the study. ExbB, atpG, pnp, and yaeA mutants caused no mortality when administered at a dose of 1010 CFU intranasally. FkpA and tig mutant groups had one death each and the HI0379 group had four deaths. wildtype LD50 using this model was generally 1 multiply 107 CFU indicating that each of these mutants is at least 100 fold attenuated.

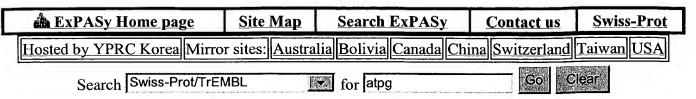
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WORLD INTELLECTUAL PROPERTY ORGANIZATION International Bureau



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

51) International Patent Classification 7:		(11) International Publication Number: WO 00/61724
C12N 1/21, C07K 14/285, A61K 35/74, 39/02, C12N 15/63, 15/31, C07K 16/12, C12Q 1/18	A2	(43) International Publication Date: 19 October 2000 (19.10.00
21) International Application Number: PCT/U;	S00/092	8 (81) Designated States: AE, AG, AL, AM, AT, AU, AZ, BA, BE
22) International Filing Date: 6 April 2000	(06.04.0	BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM
30) Priority Data: 60/128,689 9 April 1999 (09.04.99) 60/153,453 10 September 1999 (10.09. 71) Applicant: PHARMACIA & UPJOHN, INC. [US	99) t	LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ UA, UG, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian pater (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European pater (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, C
Henrietta Street, Kalamazoo, MI 49001 (US).	, 00,	CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).
72) Inventors: LOWERY, David, E.; 1207 Woodla Portage, MI 49024 (US). FULLER, Troy, E.; 11 field Drive, Battle Creek, MI 49014 (US). KI Michael, J.; 2364 Quincy Avenue, Portage, MI 49	II Dreat ENNED	n- Published Y, Without international search report and to be republished
74) Agent: WILLIAMS, Joseph, A., Jr.; Marshall, Gerstein, Murray & Borun, 6300 Sears Tower, Wacker Drive, Chicago, IL 60606-6402 (US).		
(54) Title: ANTI-BACTERIAL VACCINE COMPOSIT	TONE	
34) Tide: ANTI-BACTERIAL VACCINE COMPOSIT	IONS	
(57) Abstract	10113	
(57) Abstract	ied, the	eby allowing the identification of novel anti-bacterial agents that targe el gram negative bacterial mutants useful in vaccines.
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Entry information

Entry name

ATPG PASMU

Primary accession number

Q9L6B6

Secondary accession numbers

None

Entered in Swiss-Prot in

Release 40, October 2001

Sequence was last modified in

Release 40, October 2001 Release 41, February 2003

Annotations were last modified in

Name and origin of the protein

Protein name

ATP synthase gamma chain

Synonym

EC 3.6.3.14

Gene name

ATPG or PM1493

From

Pasteurella multocida [TaxID: 747]

Taxonomy

Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;

Pasteurellaceae; Pasteurella.

References

[1] SEQUENCE FROM NUCLEIC ACID.

Fuller T.E., Kennedy M.J., Lowery D.E.;

"Identification of Pasteurella multocida virulence genes in a septicemic mouse model using signature-tagged mutagenesis.";

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

[2] SEQUENCE FROM NUCLEIC ACID.

STRAIN=Pm70:

MEDLINE=21145866; PubMed=11248100; [NCBI, ExPASy, EBI, Israel, Japan]

May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;

"Complete genomic sequence of Pasteurella multocida Pm70.";

Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

Comments

• FUNCTION: Produces ATP from ADP in the presence of a proton gradient across the membrane.

The gamma chain is believed to be important in regulating ATPase activity and the flow of protons through the CF(0) complex.

- CATALYTIC ACTIVITY: ATP + $H_2O + H^+(In) = ADP + phosphate + H^+(Out)$.
- **SUBUNIT**: F-type ATPases have 2 components, CF(1) the catalytic core and CF(0) the membrane proton channel. CF(1) has five subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon (1). CF(0) has three main subunits: a, b and c.
- SIMILARITY: Belongs to the ATPase gamma chain family.

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Cross-references

EMBL	AF237922; AAF68408.1; [EMBL / GenBank / DDBJ] [CoDingSequence] AE006186; AAK03577.1; [EMBL / GenBank / DDBJ] [CoDingSequence]
CMR	Q9L6B6; PM1493.
InterPro	IPR000131; ATPase_gamma. Graphical view of domain structure.
Pfam	PF00231; ATP-synt; 1. Pfam graphical view of domain structure.
PRINTS	PR00126; ATPASEGAMMA.
TIGRFAMs	TIGR01146; ATPsyn_F1gamma; 1.
PROSITE	PS00153; ATPASE_GAMMA; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
BLOCKS	<u>Q9L6B6</u> .
ProtoNet	Q9L6B6.
ProtoMap	Q9L6B6.
PRESAGE	Q9L6B6.
DIP	Q9L6B6.
ModBase	Q9L6B6.
SMR	Q9L6B6; 1E1E862B4EEA9F70.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.

Keywords

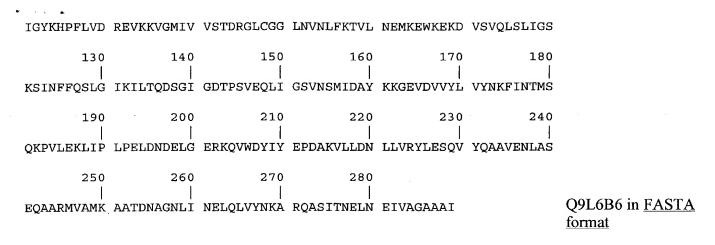
ATP synthesis; CF(1); Hydrogen ion transport; Hydrolase; Complete proteome.

Features

None

Sequence information

Molecular weight: 32095 CRC64: 1E1E862B4EEA9F70 [This is a checksum on the Length: 289 $\mathbf{A}\mathbf{A}$ Da sequence] 10 20 30 40 50 60 MAGAKEIRTK IASVKSTOKI TKAMEMVAAS KMRKTOERMS SSRPYSETIR NVISHVSKAT 70 80 90 110 100 120 1



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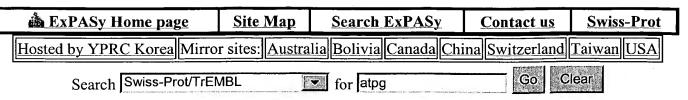


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Entry information

Entry name ATPG_PASMU

Primary accession number Q9L6B6

Secondary accession numbers None

Entered in Swiss-Prot in Release 40, October 2001 Sequence was last modified in Release 40, October 2001 Annotations were last modified in Release 41, February 2003

Name and origin of the protein

Protein name ATP synthase gamma chain

Synonym **EC 3.6.3.14**

Gene name ATPG or PM1493

From Pasteurella multocida [TaxID: 747]

Taxonomy <u>Bacteria</u>; <u>Proteobacteria</u>; <u>Gammaproteobacteria</u>; <u>Pasteurellales</u>;

Pasteurellaceae; Pasteurella.

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Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

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HOBACGEN	[Family / Alignment / Tree]
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ProtoMap	<u>Q9L6B6</u> .
PRESAGE	<u>Q9L6B6</u> .
DIP	Q9L6B6.
ModBase	Q9L6B6.
SMR	Q9L6B6; 1E1E862B4EEA9F70.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.
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Keywords

ATP synthesis; CF(1); Hydrogen ion transport; Hydrolase; Complete proteome.

Features

None

Sequence information

Length: 289 Molecular weight: 32095 CRC64: 1E1E862B4EEA9F70 [This is a checksum on the sequence] $\mathbf{A}\mathbf{A}$ Da 10 20 30 50 60 MAGAKEIRTK IASVKSTOKI TKAMEMVAAS KMRKTOERMS SSRPYSETIR NVISHVSKAT 70 80 90 100 120 110

IGYKHPFLVD REVKKVGMIV VSTDRGLCGG LNVNLFKTVL NEMKEWKEKD VSVQLSLIGS 140 150 160 170 180 130 KSINFFQSLG IKILTQDSGI GDTPSVEQLI GSVNSMIDAY KKGEVDVVYL VYNKFINTMS 190 200 210 230 OKPVLEKLIP LPELDNDELG ERKQVWDYIY EPDAKVLLDN LLVRYLESQV YQAAVENLAS 250 260 270 Q9L6B6 in FASTA EOAARMVAMK AATDNAGNLI NELQLVYNKA RQASITNELN EIVAGAAAI format

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	L2	atpg or atp-g	644
	L3	L2.ti,ab,clm.	130
1	L4	L3 and pasteur\$	1
	DB=EPAB; F	PLUR=YES; OP=AND	
i i	L5	WO-200061724-A2.did.	0
	L6	BR-200009663-A.did.	0

END OF SEARCH HISTORY

0023] Any member of the <u>Pasteurellaceae</u> may be used according to the present invention. These include, without limitation members of the genus Actinobacillus, Bisgaard taxa, the genus Haemophilus, the genus Pasteurella, as well as unclassified members of the <u>Pasteurellaceae</u>, such as <u>Pasteurellaceae</u> gen. sp. CCUG28030, and <u>Pasteurellaceae</u> gen. sp. JF1390. Particularly important members of this family include P. haemolytica, P. multocida, P. pneumotropica, H. somnus, H. influenzae, H. parasuis, A. pleuropneumoniae, A. suis, and A. actinomycetemcomitans.

Brief Summary Text (22):

Described is a live vaccine against bacterial pathogens comprising a recombinant riboflavin-requiring mutant having a mutation that inactivates riboflavin biosynthesis therein. In particular, this includes bacterial pathogens in the family Pasteurellaceae, which include animal pathogens as Actinobacillus pleuropneumoniae, Actinobacillus suis, Haemophilus parasuis, Pasteurella haemolytica and Pasteurella multocida, as well as human pathogens Haemophilus influenzae and Haemophilus ducreyi.

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L1: Entry 12 of 74

File: PGPB

Sep 18, 2003

DOCUMENT-IDENTIFIER: US 20030175835 A1

TITLE: Pathogen for bacterial poultry disease

Detail Description Paragraph:

[0043] The results of tests from sections A and B in the examples (Tables 1, 2 and 3) confirms the bacteria BIV-4895; ATCC No. PTA-3667 and BIV-AVICOR; ATCC No. PTA-3668 to belong to the family <u>Pasteurellaceae</u> (Pasteurella trehalosi, which are Trehalose positive and arabinose negative), while the bacteria BIV-07990; ATCC No. PTA-3669 belong to the family Mannheimia (Mannheimia haemolytica, which are Trehalose negative and arabinose negative).

Detail Description Paragraph:

[0087] The results of tests from Section A and B (Tables 1, 2 and 3) confirms the bacteria BIV-4895; ATCC No. PTA-3667 and BIV-AVICOR; ATCC No. PTA-3668 belong to the family Pasteurellaceae, (Pasteurella trehalosi, which are Trehalose positive and and arabinose negative), while the bacteria BIV-07990; ATCC No. PTA-3669 belong to the family Mannheimia (Mannheimia haemolytica, which are Trehalose negative and arabinose negative). Identification of the Causative Agent

Summary of Invention Paragraph:

[0036] The mutant bacterium can be a <u>Pasteurellaceae</u>, e.g. the bacterium can be: Pasteurella multocida, Pasteurella haemolytica, Pasteurella anatipestifer or Actinobacillus pleuropneumoniae; advantageously Pasteurella multocida.

Summary of Invention Paragraph:

[0062] The invention concerns micro-organisms, such as bacteria, e.g., gram negative bacteria, such as bacteria of the <u>Pasteurellaceae</u> family, for instance, Pasteurella multocida, Pasteurella haemolytica, Pasteurella anatipestifer and Actinobacillus pleuropneumoniae. Advantageously the bacteria are Pasteurella multocida.

Summary of Invention Paragraph:

[0106] Heterologous nucleic acid sequences which are suitable for this use in such a vector will be apparent to the skilled person (Fedorova N D and Highlander S K, Infect Immun 1997, 65(7): 2593-8) and include for example those coming from <u>Pasteurellaceae</u> family members (notably Pasteurella mutocida, Pasteurella haemolytica, Pasteurella anatipestifer, Actinobacillus pleuropneumoniae),

First Hit



L1: Entry 1 of 74

File: PGPB

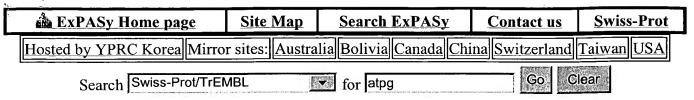
Feb 19, 2004

DOCUMENT-IDENTIFIER: US 20040033994 A1

TITLE: Use of compounds comprising a nitrogen-oxygen heterocycle

CLAIMS:

13. Use according to claim 11 for the preparation of a pharmaceutical preparation for the treatment of infections, caused by bacteria, which are selected from the group, which consists of bacteria of the family Propionibacteriaceae, in particular the genus Propiomibacterium, in particular species Propionibacterium acnes, bacteria bacteria of the family Actinomycetaceae, in particular the genus Actinomyces, bacteria of the genus Corynebacterium, in particular the species Corynebacterium diphteriae and Corynebacterium pseudotuberculosis, bacteria of the family Mycobacteriaceae, the genus Mycobacterium, in particular the species Mycobacterium leprae, Mycobacterium tuberculosis, Mycobacterium bovis and Mycobacterium avium, bacteria of the family Chlamydiaceae, in particular the species Chlamydia trachomatis and Chlamydia psittaci, bacteria of the genus Listeria, in particular the species Listeria monocytogenes, bacteria of the species Erysipelthrix rhusiopathiae, bacteria of the genus Clostridium, bacteria of the genus Yersinia, of of the species Yersinia pestis, Yersinia pseudotuberculosis, Yersinia enterocolitica enterocolitica and Yersinia ruckeri, bacteria of the family Mycoplasmataceae, of the the genera Mycoplasma and Ureaplasma, in particular the species Mycoplasma pneumoniae, bacteria of the genus Brucella, bacteria of the genus Bordetella, bacteria of the family Neisseriaceae, in particular of the genera Neisseria and Moraxella, in particular the species Neisseria meningitides, Neisseria gonorrlhoeae and Moraxella bovis, bacteria of the family Vibrionaceae, in particular of the genera Vibrio, Aeromonas, Plesiomonas and Photobacterium, in particular the species Vibrio cholerae, Vibrio anguillarum and Aeromonas salmonicidas, bacteria of the genus Camnpylobacter, in particular the species Campylobacter jejuni, Campylobacter coli and Carnpylobacter fetus, bacteria of the genus Helicobacter, in particular the the species Helicobacter pylori, bacteria of the families Spirochaetaceae and Leptospiraceae, in particular the genera Treponema, Borrelia and Leptospira, in particular Borrelia burgdorferi, bacteria of the genus Actinobacillus, bacteria of the family Legionellaceae, the genus Legionella, bacteria of the family Rickettsiaceae and family Bartonellaceae, bacteria of the genera Nocardia and Rhodococcus, bacteria of the genus Dermatophilus, bacteria of the family Pseudomonadaceae, in particular the genera Pseudomonas and Xanthomonas, bacteria of the family Enterobacteriaceae, in particular the genera Escherichia, Klebsiella, Proteus, Providencia, Salmonella, Serratia and Shigella, bacteria of the family Pasteurellaceae, in particular the genus Haemophilus, bacteria of the family Micrococcaceae, in particular the genera Micrococcus and Staphylococcus, bacteria of the family Streptococcaceae, in particular the genera Streptococcus and Enterococcus and bacteria of the family Bacillaceae, in particular the genera Bacillus and Clostridium, and in the eradication of Helicobacter in ulcers of the gastrointestinal tract.



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Entry information

Entry name

ATPG HAEIN

Primary accession number

P43716

Secondary accession numbers

None

Entered in Swiss-Prot in

Release 32, November 1995

Sequence was last modified in

Release 32, November 1995

Annotations were last modified in

Release 41, February 2003

Name and origin of the protein

Protein name

ATP synthase gamma chain

Synonym

EC <u>3.6.3.14</u>

Gene name

ATPG or HI0480

From

Haemophilus influenzae [TaxID: 727]

Taxonomy

Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;

Pasteurellaceae; Haemophilus.

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=Rd/KW20/ATCC 51907;

MEDLINE=95350630; PubMed=7542800; [NCBI, ExPASy, EBI, Israel, Japan]

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A.,

Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M.,

Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L.,

McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;

"Whole-genome random sequencing and assembly of Haemophilus influenzae Rd."; Science 269:496-512(1995).

Comments

• FUNCTION: Produces ATP from ADP in the presence of a proton gradient across the membrane.

The gamma chain is believed to be important in regulating ATPase activity and the flow of protons through the CF(0) complex.

- CATALYTIC ACTIVITY: ATP + $H_2O + H^+(In) = ADP + phosphate + H^+(Out)$.
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Cross-references

EMBL	U32730; AAC22138.1;[EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	<u>E64071</u> ; E64071.
TIGR	<u>HI0480;</u>
InterPro	IPR000131; ATPase_gamma. Graphical view of domain structure.
Pfam	PF00231; ATP-synt; 1. Pfam graphical view of domain structure.
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ModBase	<u>P43716</u> .
SMR	P43716; 622CBA682F37FD00.
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View cluster of proteins with at least 50% / 90% identity.

IGYKHPFLVE REVKKIGILV ISTDRGMCGG LNVNLFKTTL NQIKNWKEQN ISTDLGLIGS 130 140 150 160 170 180 KGISFFRSFG FNIKGQLSGL GDTPALEELI GVANTMFDAY RNGEIDAVYI AYNKFVNTMS 190 200 210 220 230 QKPVVQQLVP LPESKDDHLN ERQQTWDYLY EPEPKVLLDS LLVRYLESQI YQAVVDNVAS 250 260 270 280 P43716 in <u>FASTA</u> EQAARMVAMK AATDNAGNLI NDLRLVYNKA RQASITNELN EIVAGAAAI **format**

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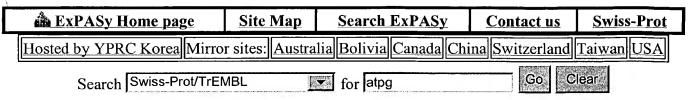


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Entry information

Entry name Primary accession number Secondary accession numbers Entered in Swiss-Prot in Sequence was last modified in Annotations were last modified in

None Release 32, November 1995

ATPG HAEIN

P43716

Release 32, November 1995

Release 41, February 2003

Name and origin of the protein

Protein name

ATP synthase gamm'a chain

Synonym

EC 3.6.3.14

Gene name

ATPG or HI0480

From Taxonomy Haemophilus influenzae [TaxID: 727]

Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;

Pasteurellaceae; Haemophilus.

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=Rd / KW20 / ATCC 51907;

MEDLINE=95350630; PubMed=7542800; [NCBI, ExPASy, EBI, Israel, Japan]

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L.,

McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;

"Whole-genome random sequencing and assembly of Haemophilus influenzae Rd."; Science 269:496-512(1995).

Comments

• FUNCTION: Produces ATP from ADP in the presence of a proton gradient across the membrane.

The gamma chain is believed to be important in regulating ATPase activity and the flow of protons through the CF(0) complex.

- CATALYTIC ACTIVITY: ATP + $H_2O + H^+(In) = ADP + phosphate + H^+(Out)$.
- **SUBUNIT**: F-type ATPases have 2 components, CF(1) the catalytic core and CF(0) the membrane proton channel. CF(1) has five subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon (1). CF(0) has three main subunits: a, b and c.
- SIMILARITY: Belongs to the ATPase gamma chain family.

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Cross-references

EMBL	U32730; AAC22138.1;[EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	<u>E64071</u> ; E64071.
TIGR	<u>HI0480;</u>
InterPro	IPR000131; ATPase_gamma. Graphical view of domain structure.
Pfam	PF00231; ATP-synt; 1. Pfam graphical view of domain structure.
PRINTS	PR00126; ATPASEGAMMA.
TIGRFAMs	TIGR01146; ATPsyn_F1gamma; 1.
PROSITE	PS00153; ATPASE_GAMMA; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
BLOCKS	<u>P43716</u> .
ProtoNet	<u>P43716</u> .
ProtoMap	<u>P43716</u> .
PRESAGE	<u>P43716</u> .
ĎIP	<u>P43716</u> .
ModBase	<u>P43716</u> .
SMR	P43716; 622CBA682F37FD00.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.
Transport and a	

Keywords

ATP synthesis; CF(1); Hydrogen ion transport; Hydrolase; Complete proteome.

Features

None

Sequence information

Length: 289 Molecular weight: 32069 CRC64: 622CBA682F37FD00 [This is a checksum on the AA Da sequence] 10 20 30 50 60 MAGAKEIKTK IASVQSTQKI TKAMEMVATS KMRKTQDRMA ASRPYSETIR NVISHVSKAS 70 80 90 100 110 120

IGYKHPFLVE REVKKIGILV ISTDRGMCGG LNVNLFKTTL NQIKNWKEQN ISTDLGLIGS 170 130 140 150 160 KGISFFRSFG FNIKGQLSGL GDTPALEELI GVANTMFDAY RNGEIDAVYI AYNKFVNTMS 190 200 210 220 230 240 QKPVVQQLVP LPESKDDHLN ERQQTWDYLY EPEPKVLLDS LLVRYLESQI YQAVVDNVAS 250 260 270 280 P43716 in <u>FASTA</u> EQAARMVAMK AATDNAGNLI NDLRLVYNKA RQASITNELN EIVAGAAAI format

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Sequence analysis tools: <u>ProtParam</u>, <u>ProtScale</u>, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

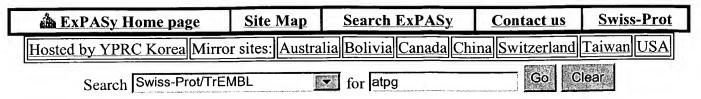


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Q9L6B6

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Entry information

Entry name ATPG PASMU

Primary accession number Q9L6B6

Secondary accession numbers None

Entered in Swiss-Prot in Release 40, October 2001
Sequence was last modified in Release 40, October 2001
Annotations were last modified in Release 41, February 2003

Name and origin of the protein

Protein name ATP synthase gamma chain

Synonym **EC** <u>3.6.3.14</u>

Gene name ATPG or PM1493

From Pasteurella multocida [TaxID: 747]

Taxonomy <u>Bacteria</u>; <u>Proteobacteria</u>; <u>Gammaproteobacteria</u>; <u>Pasteurellales</u>;

Pasteurellaceae; Pasteurella.

References

[1] SEQUENCE FROM NUCLEIC ACID.

Fuller T.E., Kennedy M.J., Lowery D.E.;

"Identification of Pasteurella multocida virulence genes in a septicemic mouse model using signature-tagged mutagenesis.";

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

[2] SEQUENCE FROM NUCLEIC ACID.

STRAIN=Pm70;

MEDLINE=21145866; PubMed=11248100; [NCBI, ExPASy, EBI, Israel, Japan]

May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;

"Complete genomic sequence of Pasteurella multocida Pm70.";

Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

Comments

• FUNCTION: Produces ATP from ADP in the presence of a proton gradient across the membrane.

The gamma chain is believed to be important in regulating ATPase activity and the flow of protons through the CF(0) complex.

- CATALYTIC ACTIVITY: ATP + H₂O + H⁺(In) = ADP + phosphate + H⁺(Out).
- **SUBUNIT**: F-type ATPases have 2 components, CF(1) the catalytic core and CF(0) the membrane proton channel. CF(1) has five subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon (1). CF(0) has three main subunits: a, b and c.
- SIMILARITY: Belongs to the ATPase gamma chain family.

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Cross-references

EMBL	AF237922; AAF68408.1; [EMBL / GenBank / DDBJ] [CoDingSequence] AE006186; AAK03577.1; [EMBL / GenBank / DDBJ] [CoDingSequence]
CMR	Q9L6B6; PM1493.
InterPro	IPR000131; ATPase_gamma. Graphical view of domain structure.
Pfam	PF00231; ATP-synt; 1. Pfam graphical view of domain structure.
PRINTS	PR00126; ATPASEGAMMA.
TIGRFAMs	TIGR01146; ATPsyn_F1gamma; 1.
PROSITE	PS00153; ATPASE_GAMMA; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
BLOCKS	Q9L6B6.
ProtoNet	Q9L6B6.
ProtoMap	<u>Q9L6B6</u> .
PRESAGE	Q9L6B6.
DIP	Q9L6B6.
ModBase	Q9L6B6.
SMR	Q9L6B6; 1E1E862B4EEA9F70.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.

Keywords

ATP synthesis; CF(1); Hydrogen ion transport; Hydrolase; Complete proteome.

Features

None

Sequence information

Length: 289 Molecular weight: 32095 CRC64: 1E1E862B4EEA9F70 [This is a checksum on the AA Da sequence] 10 20 30 50 60 MAGAKEIRTK IASVKSTQKI TKAMEMVAAS KMRKTQERMS SSRPYSETIR NVISHVSKAT 70 80 90 100 110 120

IGYKHPFLVD REVKKVGMIV VSTDRGLCGG LNVNLFKTVL NEMKEWKEKD VSVQLSLIGS 130 140 150 160 170 180 KSINFFQSLG IKILTQDSGI GDTPSVEQLI GSVNSMIDAY KKGEVDVVYL VYNKFINTMS 190 200 210 220 230 240 QKPVLEKLIP LPELDNDELG ERKQVWDYIY EPDAKVLLDN LLVRYLESQV YQAAVENLAS 250 260 270 280 Q9L6B6 in FASTA EQAARMVAMK AATDNAGNLI NELQLVYNKA RQASITNELN EIVAGAAAI format

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BLAST submission on **BLAST** ExPASy/SIB or at NCBI (USA)



Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

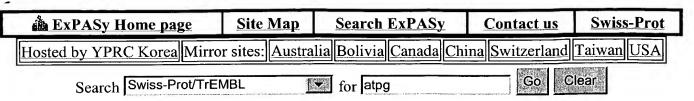


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Entry information

Entry name

Q83V88

Primary accession number

Q83V88

Secondary accession numbers

None

Entered in TrEMBL in

Release 24, June 2003

Sequence was last modified in

Release 24, June 2003

Annotations were last modified in

Release 25, October 2003

Name and origin of the protein

Protein name

ATP synthase F1 epsilon subunit [Fragment]

Synonyms

None

Gene name

ATPG

From

Haemophilus influenzae [TaxID: 727]

Taxonomy

Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;

Pasteurellaceae; Haemophilus.

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=1158:

MEDLINE=22683422; PubMed=12797973; [NCBI, ExPASy, EBI, Israel, Japan]

Cody A.J., Field D., Feil E.J., Stringer S., Deadman M.E., Tsolaki A.G., Gratz B., Bouchet V., Goldstein R., Hood D.W., Moxon E.R.;

"High rates of recombination in otitis media isolates of non-typeable Haemophilus influenzae."; Infect. Genet. Evol. 3:57-66(2003).

Comments

None

Cross-references

EMBL

AF535885; AAP19744.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]

GO:0016020; Cellular component: membrane (inferred from electronic annotation).

GO

GO:0015992; Biological process: proton transport (inferred from electronic

annotation).

InterPro

IPR000131; ATPase gamma.

Graphical view of domain structure.

Pfam

PF00231; ATP-synt; 1.

Pfam graphical view of domain structure.

PRINTS

PR00126; ATPASEGAMMA.

HOBACGEN

[Family / Alignment / Tree]

ProtoMap

Q83V88.

PRESAGE

Q83V88.

ModBase

Q83V88.

SMR

Q83V88; 72005BDBF7066A3E.

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UniRef

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Keywords

None

Features



Feature table viewer

Key

From To Length Description

Length: 150 AA [This is the Molecular weight: 16593 Da

NON TER

1

NON TER 150 150

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Sequence information

70

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100

110

STDRGMCGGL NVNLFKTTLN QIKNWKEQNI STDLGLIGSK GISFFRSFGF NIKGQLSGLG

90

130 140 150 DTPALEELIG VANTMFDAYR NGEIDAIYIA

80

Q83V88 in FASTA

format

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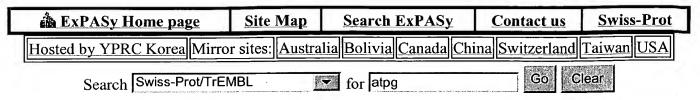


Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)





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Entry information

Entry name

Q83U83

Primary accession number

Q83U83

Secondary accession numbers

None

Entered in TrEMBL in

Release 24, June 2003

Sequence was last modified in

Release 24, June 2003

Annotations were last modified in

Release 25, October 2003

Name and origin of the protein

Protein name

ATP synthase F1 epsilon subunit [Fragment]

Synonyms

None

~

. ___

Gene name

ATPG

From

Haemophilus influenzae [TaxID: 727]

Taxonomy

Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;

Pasteurellaceae; Haemophilus.

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=1200, 1207, 1231, 1233, 1268, and 176;

MEDLINE=22683422; PubMed=12797973; [NCBI, ExPASy, EBI, Israel, Japan]

Cody A.J., Field D., Feil E.J., Stringer S., Deadman M.E., Tsolaki A.G., Gratz B., Bouchet V., Goldstein R., Hood D.W., Moxon E.R.;

"High rates of recombination in otitis media isolates of non-typeable Haemophilus influenzae."; Infect. Genet. Evol. 3:57-66(2003).

Comments

None

EMBL

Cross-references

AF535887; AAP19746.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]

AF535888; AAP19747.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]

AF535889; AAP19748.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence] AF535890; AAP19749.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]

AF535892; AAP19751.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]

AF535894; AAP19753.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]

GO:0016020; Cellular component: membrane (inferred from electronic annotation).

GO

GO:0015992; Biological process: proton transport (inferred from electronic

annotation).

InterPro

IPR000131; ATPase gamma.

Graphical view of domain structure.

PF00231; ATP-synt; 1.

Pfam

Pfam graphical view of domain structure.

PRINTS

PR00126; ATPASEGAMMA.

HOBACGEN

[Family / Alignment / Tree]

ProtoMap

Q83U83.

PRESAGE

Q83U83.

ModBase

Q83U83.

SMR

Q83U83; 72004DAA90066A3E.

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UniRef

View cluster of proteins with at least 50% / 90% identity.

Keywords

None

Features



Feature table viewer

Key From To Length Description

NON_TER 1 1 NON_TER 150 150

Sequence information

Length: 150 AA [This is the Molecular weight: 16621 Da CRC64: **72004DAA90066A3E** [This is length of the partial This is the MW of the partial a checksum on the sequence] sequence] sequence] 30 50 20 40 60 KAMEMVATSK MRKTQDRMAA SRPYSETIRN VISHVSKASI GYKHPFLVER EVKKIGILVI 70 80 90 100 110 STDRGMCGGL NVNLFKTTLN QIKNWKEQNI STDLGLIGSK GISFFRSFGF NIKGQLSGLG 130 140 DTPVLEELIG VANTMFDAYR NGEIDAIYIA Q83U83 in FASTA format

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BLAST submission on

Sequence analysis tools: ProtParam, ProtScale,

ExPASy/SIB BLAST or at NCBI (USA)



Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

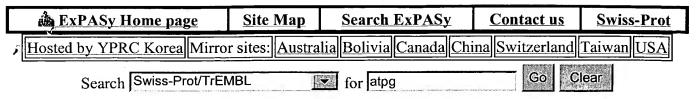


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Entry information

Entry name

Q83U82

Primary accession number

Q83U82

Secondary accession numbers

None

Entered in TrEMBL in

Release 24, June 2003

Sequence was last modified in

Release 24, June 2003

Annotations were last modified in

Release 25, October 2003

Name and origin of the protein

Protein name

ATP synthase F1 epsilon subunit [Fragment]

Synonyms

None

Gene name

ATPG

From

Haemophilus influenzae [TaxID: 727]

Taxonomy

Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;

Pasteurellaceae; Haemophilus.

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=1124, 375, 477, and 723;

MEDLINE=22683422; PubMed=12797973; [NCBI, ExPASy, EBI, Israel, Japan]

Cody A.J., Field D., Feil E.J., Stringer S., Deadman M.E., Tsolaki A.G., Gratz B., Bouchet V., Goldstein R., Hood D.W., Moxon E.R.;

"High rates of recombination in otitis media isolates of non-typeable Haemophilus influenzae."; Infect. Genet. Evol. 3:57-66(2003).

Comments

None

Cross-references

EMBL

AF535898; AAP19757.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]

AF535901; AAP19760.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]

GO:0016020; Cellular component: membrane (inferred from electronic annotation).

<u>GO:0015992</u>; Biological process: proton transport (inferred from electronic annotation).

annotation).

GO .

InterPro IPR000131; ATPase_gamma.

Graphical view of domain structure.

PF00231; ATP-synt; 1.

Pfam Pfam graphical view of domain structure.

PRINTS PR00126; ATPASEGAMMA. HOBACGEN [Family / Alignment / Tree]

ProtoMap Q83U82.
PRESAGE Q83U82.
ModBase Q83U82.

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UniRef View cluster of proteins with at least 50% / 90% identity.

Keywords

None

Features



Feature table viewer

Key From To Length Description

NON_TER 1 1 1 NON_TER 150 150

Sequence information

Length: 150 AA [This is the Molecular weight: 16579 Da CRC64: 72005BC967066A3E [This is length of the partial This is the MW of the partial a checksum on the sequence sequence] sequence] 10 20 30 40 50 60 KAMEMVATSK MRKTQDRMAA SRPYSETIRN VISHVSKASI GYKHPFLVER EVKKIGILVI 70 80 90 100 110 120 STDRGMCGGL NVNLFKTTLN QIKNWKEQNI STDLGLIGSK GISFFRSFGF NIKGOLSGLG 130 140 150 Q83U82 in FASTA DTPALEELIG VANTMFDAYR NGEIDAVYIA format

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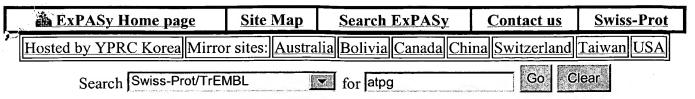
Sequence analysis tools: <u>ProtParam</u>, <u>ProtScale</u>, <u>Compute pI/Mw</u>, <u>PeptideMass</u>, <u>PeptideCutter</u>, <u>Dotlet</u> (Java)





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Note: most headings are clickable, even if they don't appear as links. They link to the <u>user manual</u> or <u>other documents</u>.

Entry information

Entry name

Q7VPP1

Primary accession number

Q7VPP1

Secondary accession numbers

None

Entered in TrEMBL in

Release 25, October 2003

Sequence was last modified in

Release 25, October 2003

Annotations were last modified in

Release 26, March 2004

Name and origin of the protein

Protein name

ATP synthase gamma chain

Synonyms

None

Gene name

ATPG or HD0009

From

Haemophilus ducreyi [TaxID: 730]

Taxonomy

Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;

Pasteurellaceae; Haemophilus.

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=35000HP / ATCC 700724;

Munson R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur R., Johnson L., Nguyen D., Wang J., Forst C., Hood L.;

"The complete genome sequence of Haemophilus ducreyi.";

Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

Comments

None

Cross-references

EMBL

AE017151; AAP95033.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]

GO:0016020; Cellular component: membrane (inferred from electronic annotation).

GO

GO:0015992; Biological process: proton transport (inferred from electronic

annotation).

CMR

Q7VPP1; HD0009.

InterPro

IPR000131; ATPase_gamma.

Graphical view of domain structure.

Pfam

PF00231; ATP-synt; 1.

Pfam graphical view of domain structure.

TIGRFAMS

TIGR01146; ATPsyn_F1gamma; 1.

PROSITE

PS00153; ATPASE_GAMMA; 1.

ProDom

[Domain structure / List of seq. sharing at least 1 domain]

HOBACGEN

[Family / Alignment / Tree]

ProtoMap

<u>Q7VPP1</u>.

PRESAGE

Q7VPP1.

ModBase

Q7VPP1.

SMR

Q7VPP1; 6CC7342402D4C977.

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UniRef

View cluster of proteins with at least 50% / 90% identity.

Keywords

Complete proteome.

Features

None

Sequence information

Molecular weight: 31953 CRC64: 6CC7342402D4C977 [This is a checksum on the Length: 288 $\mathbf{A}\mathbf{A}$ Da sequence] 40 60 10 20 30 50 MAGAKEIRTK IASVRNTOKI TKAMEMVATS KMRKTQERMA AGRPYSETIR KVISHIAKGS 70 80 90 100 110 120 IGYKHPFLIE RDVKKVGYLV ISTDRGLCGG LNINLFKTTL NEFKAWKDKD VSVELGLVGS 180 130 140 150 160 170 KGVSFYOSIG LKVRAHITGL GDSPEMERIV GAVNEMINAY RNGEVDMVCI AYNRFENTMS 190 200 210 220 230 240 QKTVIAQLLP LPKLENDELE TKCSWDYLYE PNPQVLLDSL LIRYLETQVY QAVVDNLASE 250 260 270 280 Q7VPP1 in FASTA QAARMVAMKA ATDNAGALID ELQLVYNKAR QASITNELNE IVAGAAAI format

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BLAST submission on ExPASy/SIB

Sequence analysis tools: <u>ProtParam</u>, <u>ProtScale</u>, <u>Compute pI/Mw</u>, <u>PeptideMass</u>, <u>PeptideCutter</u>,

BLAST

or at NCBI (USA)



Dotlet (Java)



ScanProsite, MotifScan



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